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June 18, 2004, 19:17:05; Search time 60 Seconds (without alignments) 1290.300 Million cell updates/sec
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1496
1 GSHSLRYFSTAVSRPGRGEP.....QRYTCHVQHEGLPQPLILRW 274
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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215 4 AAG64619 368 4 AAM24017 365 3 AAY6268 365 3 AAY52922 365 3 AAY52922 365 4 AAB5683 365 4 AAB5683 415 4 AAU06672 415 6 AAU06671 415 6 AAU06671 365 3 AAY68267 365 4 AAB56687 365 4 AAB56687		Нишал	Abp70088 Human NOV	Aay68268 Human leu	Aay52922 HLA-A2/A2	Aab58683 HLA-A2/A2	Aab36874 MHC class	Aaul0225 Human leu		Aaw68385 Chimeric	Aaul0224 Human par	Abu08671 Human sin	Aae36053 B2M-aTacV	Aay68272 Human leu	Aay68267 Human leu	_	_	_	Aab58687 HLA-A2/A2	Aay68275 Human leu
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AAG64618 12-SEP-2 Human ca	
12-SE Humar HLA-Í	118;
Humar HLA-1	12-SEP-2001 (first entry)
HLA-1	Human cancer cell specific HLA-F antigen SEQ ID 5.
	antigen; cancer cell specific; human.
Ношо	Homo sapiens.
JP20	JP2001095584-A.
10-A	10-APR-2001.
AX PF 30-SI	30-SEP-1999; 99JP-00279566.
PR 30-SI	30-SEP-1999; 99JP-00279566.
PA (EGAW/) PA (MEDI-) PA (KIMU/)	/) EGAWA K. -) MEDINET KK. /) KIMURA K.
	WPI; 2001-360493/38. N-PSDB; AAH45556.
AX PT Novel	cancer cell-specific HLA-F antigen useful for diagnosing cancer.
PS Claim 2;	2; Page 10-11; 12pp; Japanese.
	icer cell specific HLA-F antigen. The the antigen, and a method for the
	preparation of the cancer cell specific HLA-F antigen. The antigen may be
	used in a method to diagnose cancer, in which the protein is used to
CC dete	Or the patrent: ine Ta-F antiden of the
XX SQ Sequence	nce 274 AA;
Query Match Best Local Matches 27	Query Match Best Local Similarity 100.0%; Pred. No. 1.3e-133; Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps
ò	1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 60

This invention relates to a cancer cell specific HIA-F antigen. The invention includes DNA encoding the antigen, and a method for the preparation of the cancer cell specific HIA-F antigen. The antigen may be used in a method to diagnose cancer, in which the protein is used to detect anti-HIA-F antibodies in bodily fluids of the patient. The present sequence represents the cancer cell-specific HIA-F antigen of the 120 120 KDYISLNEDLRSWTAADTVAQITQRFYBAEBYAEBFRTYLBGBCLBLLRRYLBNGKETLQ 180 KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQ 180 240 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT 240 Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer. EWTTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT Human cancer cell specific HLA-F antigen SEQ ID FORWAAVVVPSGEEGRYTCHVQHEGLPQPLILRW 274 FOKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 274 HLA-F antigen; cancer cell specific; human. Disclosure; Page 9-10; 12pp; Japanese. AAG64617 standard; protein; 362 99JP-00279566. 99JP-00279566 (first entry) 2001-360493/38. EGAWA K. MEDINET KK. (MEDI-) MEDINET KF (KIMU/) KIMURA K. N-PSDB; AAH45555 Sequence 362 AA; JP2001095584-A. 30-SEP-1999; Homo sapiens 30-SEP-1999; 12-SEP-2001 10-APR-2001. invention 121 121 181 241 6 61 181 (EGAW/) 셤 ò ద ò g 셤 DP ò ò

Ovarian tumour marker gene; human; overexpression; upregulation; epithelial tumour; cancer; diagnosis; prognosis; disease monitoring; identification; serous cystadenoma; borderline serous tumour; serous cystadenoma; borderline serous cystadenoma; mucinous cystadenocarcinoma; mucinous cystadenocarcinoma; mucinous cystadenoma; borderline mucinous tumour; endometrioid carcinoma; undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma; adenofibroma; penner tumour; serial analysis of gene expression; SAGE; immune response pathway; cell proliferation regulation; protein folding; membrane localised; secreted; therapeutic target; cytostatic; HLA-Cw ovarian tumour marker protein, SEQ ID NO:82. (USSH ) US DEPT HEALTH & HUMAN SERVICES ABB50296 standard; protein; 362 AA 03-APR-2001; 2001WO-US010947. 03-APR-2000; 2000US-0194336P. (first entry) gene therapy; vaccine WO200175177-A2. sapiens. 08-FEB-2002 11-OCT-2001. ABB50296; Homo ABB50296 

202 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLIWORDGEEOTODTELVETRPAGDGT 261

181

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FORWAAVVVPSGEEORYTCHVQHEGLPOPLILRW 274 262 FQKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 295

241

82 EWTTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 141

KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEPRTYLEGECLELLRRYLENGKETLO RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT

The invention relates to methods for diagnosing and prognosing ovarian tumours in an individual via the detection and measurement of the expression of ovarian tumour marker genes (ABA831081-ABA83122, ABA83180, ABA831812 and ABA83184) or segments thereof (ABA83123-ABA83186, ABA83181 and ABA83183). The methods of the invention are useful for detecting an ovarian tumour in a patient, for identifying an individual at increased risk for developing ovarian cancer, in prognostic tests for monitoring a patient in remission from ovarian cancer and in tests for monitoring disease status in a patient being treated for ovarian cancer. The methods can additionally be used to identify a particular tumour as being an ovarian tumour (i.e., an epithelial ovarian tumour selected from serous cystadenoma, borderline serous tumour, serous cystadenoma, Detecting and identifying ovarian tumor, identifying increased risk for developing ovarian cancer, and determining effectiveness of ovarian cancer treatment, by measuring expression level of ovarian tumor marker 23; Page 126-127; 140pp; English Claim

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Length 362; Indels 9

EWTTGYAKANAQTDRVALRNLLRRYNQSBAGSHTLQGNNGCDMGPDGRLLRGYHQHAYDG 120

61

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22 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 81

1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW

100.0%; Score 1496; DB 4; 100.0%; Pred. No. 1.9e-133; iive 0; Mismatches 0;

274; Conservative

Similarity

Query Match

Best Local Matches

Sherman-Baust CA, Pizer ES, Hough CD;

WPI; 2001-626450/72. N-PSDB; ABA83122.

Morin PJ,

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mucinous cystadenoma, borderline mucinous tumour, mucinous cystadenoma, endometrioid carcinoma, undifferentiated carcinoma, clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner tumour. The ovarian tumour marker genes of the invention were identified using SAGE (serial analysis of gene expression) and were found to be overexpressed in a broad variety of ovarian epithelial tumour cells relative to normal ovarian epithelial ocalis. The marker genes are membrane-implicated in immune response pathways, in the regulation of cell proliferation and in protein folding, and many of these are membrane-localised or secreted. In addition to their use as diagnostic and prognostic markers, the ovarian tumour marker genes or their encoded prevention of ovarian cancer. Sequences ABBSO257,ABBSO39 represent proteins encoded by ovarian tumour marker genes of the invention
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23-AUG-2000; 2000US-00649167
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N-PSDB; AAS90913.
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                                                                                                                                                                                                                                                                      Sequence 362 AA;
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (POR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymuclectides are also used in diagnostics as expressed sequence tags for identifying expressed cartivity of (II) as useful in gene therapy techniques to restore normal cartivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in diagnostics, forensics, gene mapping, identification of mutations cand to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and and to produce other types of date and products dependent on DNA and and to produce other types of date and products dependent on DNA and and to produce other types of date and products dependent on DNA and and the printed specification, but was obtained in electronic format directly from MIPO at the printed specification, but was obtained in the printed specification.
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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ive 0; Mismatches 1; Indels
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AAP80911 standard; protein; 274 AA
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                                                                                                                                                                                                                                                                                                                                                                 AAC77607 to AAC78448 encode the human cancer associated proteins given in AAE43398 to AAB44239. The proteins can have activities based on the cissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antiathwantic; antirherary; immunomodulator; antidiabetic; antiasthmatic; antirherary; immunomodulator; cantidiabetic; antiasthmatic; antirherary; immunomodulator; coagulator; correctly; attriprotective; cardiant; thrombolytic; coagulant; correctly; assocrative; cardiant; thrombolytic; coagulant; coorropic; vasotropic; antipsoriatic and antiangiogenic. The noctropic; vasotropic; antipsoriatic and antiangiogenic. The coagulant; and longitions and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Correct immune cells, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ crejection, modulate haemosetatic or thrombolytic activity, modulate confirmation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in the exemplification of the present invention of the antibodies.
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                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer.
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allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.6%; Score 1311; DB 3; Length 2' 99.6%; Pred. No. 4.8e-116; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 2115-2116; 2352pp; English.
                                                                                                                                                                          99US-0124270P.
                                                                                                                                             08-MAR-2000; 2000WO-US005882.
                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
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Best Local Similarity 99.6
Matches 241; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the present invention
                                                                                                                                                                                                                                Ruben SM;
                                                                                                                                                                                                                                                             WPI; 2000-587533/55
                                                                                                                                                                                                                                                                            N-PSDB; AAC78195
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FR 269
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                                                                                                                                                                            12-MAR-1999;
                                                                                                                    21-SEP-2000
                                                                                                                                                                                                                                  Rosen CA,
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                                                                                                   Consensus sequence of peptides which constitute the alpha-1, alpha-2 and alpha-3 regions of a class I HLA molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New peptide corresp, to major histocompatibility antigen regions - used for modulating cytotoxic T-lymphocyte activity in e.g. transplants or auto-immune diseases.
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                                                                                                                                                                    HLA-A2 epitopes; extracellular domains alpha-1, alpha-2 and alpha-3
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82.8%; Pred. No. 4.8e-110;
ive 17; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                      "alpha-1 region"
                                                                                                                                                                                                                                                                                                                                                 "alpha-2 region"
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                                                                                                                                                                                                                                                            location/Qualifiers
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87US-00138547.
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                                                                (first entry)
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Best Local Similarity 82.8°
Matches 227; Conservative
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                                           (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-DEC-1987;
                                           25-MAR-2003
18-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                       WO8805784-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-AUG-1988
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AAP80911;
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205 RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTELVETRPAGDRT 264
                                                                                                                                                                                                               screening, diagnosis; ankylosing spondylitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       - and diagnostic reagents contg. such DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The DNA may be used as a hybridisation probe for detecting the HLA B27 gene, eg for assessing susceptibility to rheumatic disorders such as ankylosis spondylitis, or may be used to transform cells for prodn. of HLA B27. The HLA B27 may be used to detect HLA B27 antibody in human serum, or to produce mono- or polyclonal HLA B27 antibodies for use in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                     Sequence of the human histocompatibility antigen HLA B27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.1%; Score 1227.5; DB 1
82.5%; Pred. No. 5.7e-108;
ive 14; Mismatches 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 FQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRW 273
                        FORWAAVVVPSGEEQRYTCHVQHEGLPOPLILRW 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 5; 5pp; German.
                                                                                                                AAP70590 standard; protein; 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA coding for antigen HLA B27 antigen or antibody.
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                                                                                                                                                                                                                Rheumatic disorder; genetic
                                                                                                                                                                (first entry)
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Best Local Similarity 82.5
Matches 226; Conservative
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                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                   28-NOV-1985;
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                                                                                                                                                                10-APR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240
                                                                                                                                                                                                                                           Sequence encoded by genomic DNA encoding human histocompatibility antigen
                  THE DNA may be used to detect the HLA-B 27 gene (opt. mutated) in human genetic material. The HLA-B 27 may be used to detect anti-HLA-B 27 matibodies in human serum. The antibodies may be used to determine HLA-B 27 levels in human serum, eg for diagnosis of rheumatic disorders, esp. ankylosing spondylitis. (Updated on 25-MAR-2003 to correct PR field.)
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    RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA coding for human histocompatibility antigen HLA-B 27 diagnosis and antigen and antibody prodn.
                                                                                                                                                                                                                                                                                Ankylosing spondylitis; rheumatic disorder; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.1%; Score 1228; DB 1;
ilarity 82.1%; Pred. No. 5.6e-108;
Conservative 14; Mismatches 35;
                                                  FOXWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 274
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                                                                                                                                         AAP70155 standard; protein; 362
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85DE-03545576.
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                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                           (revised)
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N-PSDB; AAN70225.
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Best Local Similarity
Matches 225; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 362 AA;
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21-DEC-1985;
                                                                                                                                                                                                                                                                                                           варіепв
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                                                                                                                                                                                           25-MAR-2003
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03-APR-1991
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208 RADPPKTHYTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTELVETRPAGDRT 267
181 RADPPKAHVAHHPISDHEATLRCWALGFYPABITLTWQRDGEEQTQDTELVETRPAGDGT
                                                                                          268 FOKWAAVVVPSGEEGRYTCHVQHEGLPKPLTLRW 301
                                                                   241 FOKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 274
                                                                                                                                                                                                                                                                    (revised)
(first entry)
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Best Local Similarity 81.73
Matches 223; Conservative
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N-PSDB; AAQ12116.
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                                                                                                                                                                                                                                                                                                                           HLA-C exon Cb-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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29-AUG-1991
                                                                                                                                                                                                                                    AAR12465;
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                                                                                                                                                                                                                                                                                                                                                             Human
                                                                                                                                                                RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells corpressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to abstrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins of a nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoises; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU32910-AAU33304 represent the amino acid sequences of novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EWITGYAKANAQIDRVALRNILLRRYNQSEAGSHILQGMNGCDMGPDGRILRGYHQHAYDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 GSHSWRYFDTAMSRPGRGEPRFISVGYVDDTQPVRFDSDAASPREEPRAPMIEQEGPBYW 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
                                                                                                                                                                                              Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune stimulation; anti-inflammatory; leukaemia.
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81.0%; Pred. No. 1.4e-107;
ive 21; Mismatches 31; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; Page 683; 765pp; English.
                                                                                                                                                                Novel human secreted protein #3373.
                                                          AAU32882 standard; protein; 369 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RT;
                                                                                                                                                                                                                                                                                                                                                                                 16-APR-2001; 2001WO-US008656
                                                                                                                                                                                                                                                                                                                                                                                                                   18-APR-2000; 2000US-00552929 26-JAN-2001; 2001US-00770160
                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 369 AA;
                                                                                                                                                                                                                                                                                                             WO200179449~A2.
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                                                                                                                                18-DEC-2001
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                                                                                            AAU32882;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 RETQKYKRQAQTDRVSLRNLRGYYNQSEAGSHTLQMMFGCDLGPDGRLLRGYDQSAYDGK 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 WITGYAKANAQIDRVALRNILRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 SHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 DYISLNEDLRSWTAADTVAQITQRFYEABBYABBFRTYLEGECLELLRRYLENGKETLQR
                                                                                                                                                                                                                              leukocyte antigen; probe; major histocompatibility complex; MHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HLA-C gene, DNA probe and transformant cells - for immunisation animals and monoclonal antibody development.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80.8%; Score 1209; DB 2;
81.7%; Pred. No. 3.7e-106;
iive 18; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 QKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 274
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AAR12465 standard; protein; 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (OLYU ) OLYMPUS OPTICAL CO LTD
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DRETQXYKRQAQTDRVSLRNLRGYYNQSEAGSHIIQRMYGCDVGPDGRLLRGYDQYAYDG

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The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers.
                                                                                                                                                                                                                               Cancer associated antigen; diagnosis; research; treatment; human;
breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stockert E, Gure A, Chen Y, Gout I; Pfreundschuh M, Tureci O, Sahin U;
                                                                                                                                                                                                 Breast cancer associated antigen precursor sequence.
266 QKWAAVMVPSGEEQRYTCHVQHEGLPEPLTLRW 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 417-418; 787pp; English.
                                                                                                 AAY07033 standard; protein; 366 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                           97US-00896164.
97US-0061599P.
97US-0061765P.
97US-00948705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-00102322.
                                                                                                                                                                                                                                                                                                                                                                                                 98WO-US014679,
                                                                                                                                                                (first entry)
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Obata Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-132448/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 366 AA;
                                                                                                                                                                                                                                                                   prostate cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                           17-JUL-1997;
10-OCT-1997;
10-OCT-1997;
10-OCT-1997;
                                                                                                                                                                02-JUL-1999
                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                  WO9904265-A2
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22-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                   28-JAN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Old LJ, Sc
O'hare M,
                                                                                                                                 AAY07033;
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61 BWTTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 120

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80.6%; Score 1206; DB 2; Length 366; 81.0%; Pred. No. 7.1e-106; ive 18; Mismatches 34; Indels (

Best Local Similarity 81.0 Matches 222; Conservative

Query Match

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                                                                                                                                                                                              205 RAEHPKTHVTHHPVSDHEATLRCWALGFYPABITLTWQWDGEDQTQDTELVETRPAGDGT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polyneptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, inchinibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                     KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGGECLELLRRYLENGKETLQ
                                                                                                                                          181 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLIWQRDGEEQTQDTELVETRPAGDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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llarity 82.1%; Pred. No. 7.3e-106;
Conservative 16; Mismatches 33;
                                                                                                                                                                                                                                                                                                                     265 FQKWAAVVVPSGEEQRYTCHVQHEGLPEPLTLRW 298
                                                                                                                                                                                                                                                                                FOKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA013073 standard; protein; 374 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-FEB-2001; 2001WO-US004927.
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18-MAY-2000; 2000US-00577409.
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Best Local Simi
Matches 224;
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80.5%; Score 1204.5; 81.8%; Pred. No. 1e-1 ive 15; Mismatches

Length 374;

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204 240 264

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KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQ 180
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                                                                                       25 GSHSMRYFYTAMSRPGRGEPRFIAVGYVDDTQFVRFDSDAASPRMAPRAPWIEQEGPEYW
                                                                                                                                            EWTTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG
                                                                                                                                                                                            1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
                                                                                                                                                                                                                                RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT
                                                                                                                                                                                                                                                                                                             265 POKWAAVVVPSGEEORYTCHVOHEGLPKPLTPERW 299
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Sequence 374 AA;
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                                                225;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polyneptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, haematopoiesis regulating activity, itssue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part directly from WIFO at ftp.wipo.int/pub/published_pct_sequences
                                                   WITGYAKANAQIDRVALRNLLRRYNQSEAGSHILQGMNGCDMGPDGRLLRGYHQHAYDGK 121
                                                                     RETOKYKROAQTDRVSLRNLRGYYNQSEAGSHTLQWMYGCDLGPDGRLLRGYDQSAYDGK 153
                                                                                                      181
                                                                                                                            DYIALNEHLRSCTAADTAAQITQRKWEAARAAEQWRAYLEGTCVEWLRRYLENGKETLQR 213
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  61
                          93
                                                                                                                                                                         214 AEHPKTHVTHHPVSDHEATLRCWALGFYPAEITLIWQRDGEDQTQDTELVETRPAGDGTF
                SHSMRYFYTAVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASPRGEPRAPWVEQEGPEYWD
  SHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYWE
                                                                                                                                                        ADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGTF
                                                                                                      DYISLNEDLRSWIAADTVAQITORFYBAEFYABEFRIYLEGECLELLRRYLENGKETLOR
                                                                                                                                                                                                                                                                                                                                                                                                        Human, cytokine, cell proliferation, cell differentiation, gene the
vaccine, poptide therapy, stem cell growth factor, haematopolesis,
tissue growth factor, immunomodulatory, cancer, leukaemia,
nervous system disorders, arthritis, inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID NO 20664; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                              OKWAAVVVPSGEEQRYTCHVQHEGLPOPLILRW 274
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                                                                                                                                                                                                                                                                                                                                                                                  Human polypeptide SEQ ID NO 20664.
                                                                                                                                                                                                                                                                                                       AAO06772 standard; protein; 374
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18-MAY-2000; 2000US-00577409.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang YT, Liu C,
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The HLA class I DNA can be used a source of probes for use in DNA typing. Transformed cells, which are useful as immmunogens, can be obtained by introducing these DNAs into eucaryotic cells. (Updated on 25-MAR-2003 to
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transformed cells, used for DNA typing, as immunogens etc.
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80.3%; Pred. No. 2.1e-105;
iive 20; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Page 13; 23pp; English.
AAR03142 standard; protein; 362 AA
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                                                                                                                                                                                                             HLA-Bw52 antigen
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The invention discloses a composition comprising two or more isolated ratter human polymuclectides or a polymuclectide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polymucleotide sequence which is differentially expression of a polymucleotide sequence which is differentially compound that regulates the activity of one or more of the polymucleotides, a method for pain, a method for identifying a compound that regulates the activity of one or more of the
                                                                                                                                                                                            240
                                                   EWTTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 120
                                                                        BETGISKINIQIYRENLRIALRYYNQSEAGSHTWQTMYGCDVGPDGRLLRGHNQYAYDG 144
                                                                                                                        KDYISLNEDLRSWTAADTVAQITQRFYBABEFARTYLEGECLBLLRRYLBNGKETLQ 180
                                                                                                                                          145 KDYIALNEDLSSWTAADTAAQITQRKWEAAREAEQLRAYLBGLCVEWLRRHLENGKETLQ 204
                                                                                                                                                                                                                   New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                    84
RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, pain, neuronal tissue, gene therapy,
spinal segmental nerve injury, chronic constriction injury, CCI,
spared nerve injury, SNI, Chung.
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                                                                                                                                                                                                                                                                                                                                                                                       ADE64171 standard; protein; 362 AA
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polymclectide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CI) and spared nerve injury (SNI)) in an animal (e.g. gene the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 KDYISINEDLRSWTAADTVAQITQRFYEAEBYAEEFRTYLEGECLELLRRYLENGKETLQ 180
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es 220; Conserva
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APPLICANT: CLAYBERGER, CAROL A.
APPLICANT: KRENSKY, ALAN M.
APPLICANT: KRENSKY, ALAN M.
TITLE OF INVENTION: CYTOTXIC T-CELL LYMPHOCYTE ("CTL")
TITLE OF INVENTION: CYTOTXIC T-CELL LYMPHOCYTE ("CTL")
TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
CITY: MACHINGTON
CONTY.
CONTY: MACHINGTON
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COUTRY: USA

COMPUTER READABLE FORM:

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COMP
US-08-481-985B-101
US-08-65-23
US-08-632-255-23
US-08-370-476-97
US-08-370-476-99
US-08-370-476-100
US-08-370-476-100
US-08-370-476-100
US-09-503-444A-23
US-09-503-444A-23
US-09-481-985E-83
US-08-481-985E-83
US-08-481-985E-82
                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                             US-08-222-851-1
; Sequence 1. Application US/08222851
; Patent No. 57-23128
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 44; Conserv
   US-08-222-851-1
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Sequence 9, Appli
Sequence 8, Appli
Sequence 79, Appli
Sequence 79, Appl
Sequence 105, Appl
Sequence 105, Appl
Sequence 105, Appl
Sequence 105, Appl
Sequence 108, Appl
Sequence 108, Appl
Sequence 108, Appl
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107, App
108, App
38, Appl
97, Appl
98, Appl
99, Appl
                                                                                                           June 18, 2004, 19:28:42; Search time 22 Seconds (without alignments) 642.978 Million cell updates/sec
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Sequence
Sequence
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Sequence
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1 GSHSLRYFSTAVSRPGRGEP......QRYTCHVQHEGLPQPLILRW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Issued Patents AA:*

... /cgn2 6/ptodata2/jaa/5A_COMB.pep:*
... /cgn2 6/ptodata2/jaa/5B_COMB.pep:*
... /cgn2 6/ptodata2/jaa/6A_COMB.pep:*
... /cgn2 6/ptodata2/jaa/6B_COMB.pep:*
... /cgn2 6/ptodata2/jiaa/PCTUS COMB.pep:*
... /cgn2 6/ptodata2/jiaa/PCTUS COMB.pep:*
... /cgn2 6/ptodata2/jiaa/PCTUS COMB.pep:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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S-08-484-905-79
S-08-484-905-79
S-08-484-905-105
S-08-484-905-107
S-08-481-985B-107
S-08-481-985B-107
S-08-481-985B-107
S-08-370-476-108
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3-08-484-905-98
3-08-484-905-99
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                                                                                                                                                                                                                                                                                                 389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                  using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                               OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                 US-09-819-371-5
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Match Length
                                                                                  protein search,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                               Scoring table:
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                                                                                      protein
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                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                   Run on:
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Sequence 8, Application US/08406057;
Patent No. 585642
GENERAL INFORMATION:
APPLICANT: CAROSELLA, EDGARDO D
APPLICANT: GLUCKMAN, ELIANE
APPLICANT: GLUCKMAN, ELIANE
TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDERSS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 117;
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1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
                                                                                                                          COMPUTER READABLE FORM:

MEDLIOM TYPE: Tape
COMPUTER: IBM PC compatible
COMFUTER: IBM PC compatible
SUGUNARE: PR PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
FILING DATE: 12 corr.1997
CLASS!FICATION NUMBER: FR 94 03179
FILING DATE: 18 -MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
RESTSTRATION NUMBER: 24,618
REFERENCE/POCKET NUMBER: 24,618
RESTSTRATION NUMBER: 24,618
RESTSTRATION NUMBER: 0846-0437-0
TELECOMMUNICATION NUMBER: 0846-0437-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Tay
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTER RELease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,057
FILING DATE: 17-MAR-1995
CLASSIECATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94 03179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 ELVETRPAGDGTFOKWAAVVVPSGEEORYTCHVOHEGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 ELVETRPAGDGTFOKWAAVVVPSGEEORYTCHVOHEGLP
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100.0%; Pred. No. 4.8e-31;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (703) 413-3000
(703) 413-2220
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 39; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                        ARLINGTON
VIRGINIA
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TELEFAX: (
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                                                                                                                          Sequence 9, Application US/08406057
| Batent No. 5856442
| GENERAL INFORMATION: CAROSLIA, EDGARDO D
| APPLICANT: CAROSLIA, EDGARDO D
| APPLICANT: MOREAU, PHILIPPE
| APPLICANT: MOREAU, PHILIPPE
| APPLICANT: KIRSEBERBAUM, MAREK
| TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
| TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
| NUMBER OF SEQUENCES: 15
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT STREET: 1755 S. UBFFERSON DAVIS HIGHWAY, FOURTH FLOOR STATE: VIRGINIA
| COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFORMED BY APPLICATION US/08958316
| Sequence 9, Application US/08958316
| Patent No. 6291659
| GENERAL INFORMATION:
| APPLICANT: CAROSELA, EDGARDO D
| APPLICANT: GLUCKMAN, ELIANE
| APPLICANT: GLUCKMAN, ELIANE
| APPLICANT: KIRSZENBAUM, MAREK
| TITLE OF INVENTION: TRANSCRIETS OF THE MHC CLASS I HLA-G
| TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
| VUMBER OF SEQUENCES: 17
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.2%; Score 39; DB 2; Length 117; 100.0%; Pred. No. 4.8e-31; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Tape
COMPUT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 39; Conservative
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MOLECULE TYPE: peptide
US-08-406-057-9
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US-08-958-316-9
                                                                              RESULT 2
US-08-406-057-9
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Gaps

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GENERAL INFORMATION:
APPLICANT: Abstacked, Jean-Pierre
APPLICANT: Countisty, Philippe
TITLE OF INVENTION: Complex(MEC) Determinant and Methods for Using the
TITLE OF INVENTION: Complex(MEC) Determinant
CORRESPONDENCE ADDRESS: 127
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
ADDRESSEE: Pinnegan, Henderson, Farabow, Garrett &
APPLICATION DATA:
APPLICATION NUMBER: US 07/80444,905
FILING DATE: 15-NOV-1991
CLASSIFICATION NUMBER: 33,3345.0106-03000
FRIGHS APPLICATION NUMBER: 33,3345.0106-03000
FRIENDAM: 202-408-4000
INFORMATION FOR REQ ID NO: 79:
RELECOMMUTCATION NUMBER: 33,3345.0106-03000
INFORMATION FOR REQ ID NO: 79:
RELECOMMUTCATION NUMBER: 33,3345.0106-03000
INFORMATION FOR REQ ID NO: 79:
RELECOMMUTCATION NUMBER: 33,3345.0106-03000
INFORMATION FOR REQ ID NO: 79:
REMORTH: APPLICATION COLOR-400
INFORMATION FOR REQ ID NO: 79:
REMORTH: APPLICATION COLOR-400
INFORMATION FOR REQ ID NO: 79:
REMORTH: APPLICATION COLOR-400
INFORMATION FOR REQ ID NO: 79:
REMORTH: APPLICATION COLOR-400
INFORMATION COLOR-400
INFORMATION FOR REQ ID NO: 79:
REMORTH: APPLICATION COLOR-400
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10.9%; Score 30; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 9.4e-22;
Matches 30; Conservative 0; Mismatches 0; Indels
                                                                                       Length 145;
                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                     79 ELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 117
                                                                                                                                                                                                                                      229 ELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP
                                                                                   Score 39; DB 3; Le
Pred. No. 5.9e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   226 ODTELVETRPAGDGTFOKWAAVVVPSGEEQ 255
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                                                                                   Query Match
14.2%; Score 39; DB
Best Local Similarity 100.0%; Pred. No. 5.9
Matches 39; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-484-905-79
; Sequence 79, Application US/08484905
; Patent No. 5976551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
US-08-481-985B-79
           US-08-958-316-8
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CORRESPONDENCE ADDRESS:
ADDRESSER: OBLOW, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 2002
ZIP: 2008
ZIP: 2009
ZIP: 2008
ZIP: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08958316
Sequence 8. Application US/08958316
Sequent No. 6291659
GENERAL INFORMATION:
APPLICANT: CAROSELLA, EDGARDO D
APPLICANT: GLICKMAN, ELIANE
APPLICANT: KIRSZENBAUM, MAREK
TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 145
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14.2%; Score 39; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 5.9e-31;
Matches 39; Conservative 0; Mismatches 0;
FILING DATE: 18-MAR-1994

ATTORNEY AGENT INFORMATION:
NAME: OBLON, NORMANE: 24,618

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 846-331-0

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELERAX: (703) 413-3200

TELERAX: (703) 413-3200

TELERAX: (703) 413-220

TELERAX: 148855 OPAT UR

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids

TYPE: amino acid

TYPE: TYPE: Inear

WOLECULE TYPE: peptide
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MOLECULE TYPE: peptide
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US-08-958-316-8
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Motecz, Estelle
APPLICANT: Motecz, Estelle
APPLICANT: Motecz, Estelle
APPLICANT: Motecz, Philippe
ITTLE OF INVENTION: An Allerared Major Histocompatibility
ITTLE OF INVENTION: Determinant
TITLE OF INVENTION: Determinant
NUMBER OF SECUENCES: 127
ITTLE OF INVENTION: Determinant
NUMBER OF SECUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pinnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-315
COMPUTER READABLE FORM:
MEDIUM TYPES: RIDAPABLE FORM:
MEDIUM TYPES: READABLE FORM:
MEDIUM TYPES: READABLE FORM:
MEDIUM TYPES: READABLE FORM:
MEDIUM TYPES: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                        STREEL: # #550 CTTY: Washington
STATE: D.C.
ZITY: AMSAINGTON
STATE: D.C.
ZITY: 20005-3155
COMPUTER EXLANDALE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Dam PC Compatible
OPERATION SYSTEM: PC-DOS/MS-DCS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/117,575
FILING DATE: CLASSIFICATION NUMBER: US 08/117,575
PRIOR APPLICATION NUMBER: US 08/072,787
FILING DATE: 07-SEP-1993
PRIOR APPLICATION NUMBER: US 08/072,787
FILING DATE: 05-UN-1993
PRIOR APPLICATION NUMBER: US 07/801,816
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION NUMBER: 05-146
REGISTRATION NUMBER: 202-408-400
TELECOMMUNICATION OF 79:
SEQUENCE CRARACTERISTICS:
TENERAL 289 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 10.9%; Score 30; DB 3; Le. Best Local Similarity 100.0%; Pred. No. 9.4e-22; Matches 30; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 ODTELVETRPAGDGTFOKWAAVVVPSGEEQ 255
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                         ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: peptide US-08-370-476-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
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Sequence 79, Application US/08481985B
Patent No. Gollide
GENERAL INFORMATION:
APPLICANT: Motez, Estelle
APPLICANT: Abastado, Jean-Pierre
AUNGER, OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSES: Dunner
STRESSES: Du
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: Mottez, Estelle
APPLICANT: Mostez, Usan-Pierre
APPLICANT: Absatsado, Van-Pierre
APPLICANT: Lone, Yu-Chun
APPLICANT: Lone, Yu-Chun
APPLICANT: Casrouge, Armanda
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 289; 9.4e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          226 ODTELVETRPAGDGTFOKWAAVVVPSGEEQ 255
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10.9%; Score 30; DB
Best Local Similarity 100.0%; Pred. No. 9.4
Matches 30; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 79, Application US/08370476
Patent No. 6153408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-481-985B-79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
US-08-370-476-79
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NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33.32.
REPERBUCE/DOCKET NUMBER: 03495.0106-03000
TELECOMMUNICATION INFORMATION:
TELEPRONE: 202-408-4400
TELEPRA: 202-408-4400
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTER.STICS:
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224 QTQDTELVETRPAGDGTFQKWAAVVVPSG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         224 QIQDIELVEIRPAGDGIFQKWAAVVVPSG 252
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TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 274 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear;
MOLECULE TYPE: peptide
US-08-484-905-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide US-08-484-905-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Facquence 107, Application US/08484905

Patent No. 597651

GENERAL INFORMATION:

APPLICANT: Mottez, Estelle

APPLICANT: Abastado, Jean-Pierre

APPLICANT: Kourilsky, Philippe

TITLE OF INVENTION: Complex(MFC) Determinant and Methods for Using the

TITLE OF INVENTION: Determinant

NUMBER OF SEQUENCES: 127

CORRESPONDENCE ADDRESS:

ADDRESSE: Finnegan, Henderson, Farabow, Garrett &

ADDRESSE: Dunner

STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.6%; Score 29; DB 2; Length 274; 100.0%; Pred. No. 8.8e-21; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington
CITY: Washington
CITY: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS-/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,905
FLING DATE: 07-JUNE-1995
CLASSIFICATION 1530
PRIOR APPLICATION: 530
PRIOR APPLICATION: DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,905
FILING DATE: US-J095
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-J991
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION NUMBER: US 07/792,473
ATTOMNEY/AGENT INFORMATION:
NAME: POCLET, Jane E. R.
REGISTRATION NUMBER: 33,332
REPERENCE/DOCKET NUMBER: 33,332

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             224 QTQDTELVETRPAGDGTFQKWAAVVVPSG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224 QTQDTELVETRPAGDGTFQKWAAVVVPSG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-484-905-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
US-08-484-905-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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RESULT 11

REPREMAL INFORMATION

RESULT 11

APPLICANT: Routisty, Philippe

ITILE OF INVENTION: Complex (MHC) Determinant and Methods for Using the TITLE OF INVENTION: Complex (MHC) Determinant and Methods for Using the TITLE OF INVENTION: Octomber (MHC) Determinant

RUMBER OF EXCURRENCES: 127

RUMBER OF SEQUENCES: 127

CORRESSER: Pinnegan, Henderson, Farabow, Garrett & ADDRESSER: Pinnegan, Henderson, Farabow, Garrett & ADDRESSER: Outline

GITY: Mashington: Street, N.W., Suite 700

GITY: Mashington I Street, N.W., Suite 700

GITY: Mashington I Street, N.W., Suite 700

STREET: 2006-318

REDIUM TYPE: Flopy Disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Flopy Disk

COMPUTER: IER O'-JUNE-1995

COMPUTER: IER O'-JUNE-1995

FILING DATE: O'-JUNE-1995

FILING DATE: O'-JUNE-1995

FILING DATE: O'-LUNE-1995

FILING DATE: DEC-1991

CLASSIFICATION NUMBER: US 07/792,473

FILING DATE: DENOV-1991

CLASSIFICATION NUMBER: 03/95.0106-03000

FILING DATE: DENOV-1991

CLASSIFICATION NUMBER: 03/95.0106-03000

FELENOMUNICATION INFORMATION:

NUMBE: POFFER, Jane B. R.

RESISTRATION NUMBER: 03/95-0106-03000

TELECOMMUNICATION INFORMATION:

REPERVALION: TELECOMMUNICATION INFORMATION:

REPREMENT: POFFER 100-4000
                                                         ö
                                                            Gaps
                                                            .
0
   Length 274;
                                                         Indels
10.6%; Score 29; DB 2; Le
100.0%; Pred. No. 8.8e-21;
:ive 0; Mismatches 0;
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GENERAL INFORMATION
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US-08-481-985B-108
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                                                                           Gaps
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APPLICANT: Abastado, Jean-Pierre
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Moutez, Phillipe
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: Durner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Eloppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Petentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,985B
FILING DATE: 05-DEC-1991
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION NUMBER: 25,146
REGISTRATION NUMBER: 25,146
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0106-04000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 020-408-4000
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0
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                       Length 274;
                                                                         Indels
                          10.6%; Score 29; DB 2; Le
llarity 100.0%; Pred. No. 8.8e-21;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 QIQDIELVEIRPAGDGIFQKWAAVVVPSG 252
                                                                                                                           224 QTODTELVETRPAGDGTFOKWAAVVVPSG 252
                                                                                                                                                                       224 OTODTELVETRPAGDGTFOKWAAVVVPSG 252
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                                                                                                                                                                                                                                                RESULT 12
US-08-481-985B-105
; Sequence 105, Application US/08481985B
; Patent No. 6011146
; PADERAL INFORMATION:
APPLICANT: Mottez, Estelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear, MOLECULE TYPE: peptide US-08-481-985B-105
                            Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
US-08-481-985B-107
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APPLICANT: Mostea Carlie
APPLICANT: Mostea Carlie
APPLICANT: Mostea Carlie
APPLICANT: Mostea Carlie
APPLICANT: Mostadod, Jean-Fierre
APPLICANT: Mostadod, Jean-Fierre
APPLICANT: Mostadod, Jean-Fierre
ADDRESSE: Pinnegan, Henderson, Farabow, Garrett &
ADDRESSE: Pinnegan, Henderson, Farabow, Garrett &
ADDRESSE: Dunnegan, Henderson, 188
APPLICANTON NUMBER: US 07/792.473
APPLICANTON HENDERSE: US 07/792.473
APPLICANTON NUMBER: US 07/792.473
APPLICANT NUMBER:
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Search completed: June 18, 2004, 19:32:29 Job time : 23 secs
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Best Local Similarity 100.
Matches 29; Conservative
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MOLECULE TYPE: peptide
US-08-370-476-105
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: DC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,985B
FILING DATE: 07-JUN-1995
CLASSIFICATION DATE: US/08/481,985B
FILING DATE: 05-DEC-1991
CLASSIFICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 435
ATTORNEY/AGRAT INFORMATION:
NAME: MAYERS, KENNECH US: AREFRENCE/DOCKET NUMBER: 03495.0106-04000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAK: 202-408-4000
INFORMATION FOR SEQ ID NO: 108:
CRAFFERENCE/CORTENTION OF 108:
TELEPRAK: 274 amino acids
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CITY: Washington
STATE: D.C.
ZIATE: D.C.
ZIATE: D.C.
ZONFUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/370,476
FILING DATE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 274 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: peptide US-08-481-9858-108
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US-08-370-476-105
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Gaps
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FILING DATE: 07-SEP-1993
APPLICATION NUMBER: US 08/072,787
FILING DATE: 06-JUN-1993
BRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05243.0001-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LEMENTH: 274 amilio acids
TYPE: amilio acids
TYPE: amilio acids
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Sequence 1, Application US/08222851
Patent No. 5723128
GENERAL INFORMATION:
APPLICANT: CLAYBERGER, CAROL A. APPLICANT: KRENSKY, ALAN M. APPLICANT: PARHAM, PETER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                274 amino acids
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US-08-222-851-1
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Sequence 9
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1. /ogn2 6/ptodata/2/iaa/5A_COMB.pep:*

2. /ogn2 6/ptodata/2/iaa/5B_COMB.pep:*

3. /ogn2 6/ptodata/2/iaa/6A_COMB.pep:*

4. /ogn2 6/ptodata/2/iaa/6B_COMB.pep:*

5. /ogn2 6/ptodata/2/iaa/PoTUS COMB.pep:*

5. /ogn2 6/ptodata/2/iaa/PoTUS COMB.pep:*

5. /ogn2 6/ptodata/2/iaa/PoTUS COMB.pep:*

5. /ogn2 6/ptodata/2/iaa/PoTUS COMB.pep:*
                         GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-08-481-905-100

US-08-834-491A-23

US-08-834-491A-23

US-08-89-119-38

US-08-89-119-38

US-08-484-905-104

US-08-484-905-104

US-08-481-995-104

US-08-481-995-104

US-08-481-995-108

US-08-481-995-97

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Maximum Match 100%
Listing first 45 summaries
                                                                                                                         - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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1496
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")
TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")
TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, STE 5500
CITY: MASHINGTON
CITY: WASHINGTON
CITY: BASHINGTON
STRATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BW PC compatible
COMPUTER: B
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US-08-370-476-105
US-08-484-905-106
US-08-370-476-105
US-08-481-905-103
US-08-481-905-103
US-08-481-905-103
US-08-481-905-102
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US-08-81-905-101
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US-08-91-905-101
US-08-91-905-101
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121 KDYISLNEDIRSWTAADTVAQITQRFYEAEEFRTYLEGECLELLRRYLENGKETLQ 180
                                                                                                                                                                                                                                                                          181 RADPPKAHVAHHPISDHEATLRCWALGFYPABITLTWQRDGEEQTQDTBLVETRPAGDGT 240
                                                                                                                   61 EWTTGYAKANAQTDRVALRNILRRYNQSEAGSHTLOGMNGCDMGPDGRLLRGYHQHAYDG 120
                                                                                                                                                          85 DGETRKVKAHSQTHRVDLSTLRGYYNQSEAGSHTVQRMFGCDVGSDGRFLRGYHQYAYDG 144
                                25 GSHSKRYFYTSVSRPGRGEPRFIAVGYVDDTOFVRFDSDAASQRMEPRAPWIEQEGPEYW
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GSHSLRYFSTAVSRPGRGEPRYLAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
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Sequence 100, Application US/08481985B

Patent No. 601146

GENERAL INFORMATION:

APPLICANT: Abastado, Jean-Pierre

APPLICANT: Abastado, Jean-Pierre

APPLICANT: Abastado, Jean-Pierre

APPLICANT: Koutilsky, Phillipe

TITLE OF INVENTION: Altered Major Histocompatibility Complex

TITLE OF INVENTION: Altered Major Histocompatible

CORRESORDENCE: Planegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner

STREET: 1300 I Street, N.W., Suite 700

CITY: Washington

STREET: 1300 I Street, N.W., Suite 700

CITY: Washington

STREET: BROOF I Street, N.W., Suite 700

CITY: Washington

STREET: 1800 I Street, N.W., Suite 700

CITY: Washington

STREET: 1800 I Street, N.W., Suite 700

CITY: Washington

STREET: 1800 I Street, N.W., Suite 700

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STREET: 1800 I Street, N.W., Suite 700

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STREET: 1800 I Street, N.W., Suite 700

CITY: Washington

STREET: 1800 I Street, N.W., Suite 700

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Pred. No. 1e-104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              265 FÓKWAAVVVPSGOEÓRÝTCHVOHEGLPKPLTLPW 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
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ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0106-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.18;
76.68;
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS LENGTH: 365 amino aci
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Best Local Similarity
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US-08-481-985B-100
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                                                                             KDYISINEDIRSWTAADTVAQITQRFYBAEEYAEEFRTYLEGECLELLRRYLENGKETLQ 180
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                                                                                                                                                                                                                                                                                    181 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLIWQRDGEEQTQDTELVETRPAGDGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mottez, Estelle
APPLICANT: Mottez, Philippe
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: Complex (MHC) Determinant and Methods for Using the
TITLE OF INVENTION: Determinant
NUMBER OF INVENTION: Determinant
CORRESPONDENCE: 127
CORRESPONDENCE ADDRESS:
                                         EWITGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner STREAT: 1300 I Street, N.W., Suite 700 CITY: 1300 I Street, N.W., Suite 700 CITY: 2006-3315 COMPUTER READBLE FORM: MEDIUM TYPE: Floppy Disk COMPUTER, IBM PC compatible OPERATING SYSTEM: PC-DOS-/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,905 FILING DATE: 07-UUNE-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; L.
1e-104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 07-UNE-1995
CLASSIFICATION: 530
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: POTTET INFORMATION:
NAME: POTTET JAINER: 33,332
REGISTRATION NUMBER: 33,332
REGISTRATION NUMBER: 33,332
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 03495.0106-TELEPHONE: 202-498-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 100, Application US/08484905
Patent No. 5976551
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 76.6
Matches 210, Conservative
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Query Match
Best Local Similarity 77.09
Matches 211; Conservative
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STATE:
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                                                                                                                                                                                                                                                                                                                                                               KDYISLNEDLRSWTAADTVAQITQRFYEAEBYAEBFRTYLEGGECLELLRRYLENGKETLQ 180
                                                                                                                                                                                                                                                                                                                                                                                                     181 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT
                                                                        1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
                                                                                                                  25 GSHSMRYFYTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQEGPEYW
   Gaps
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   42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23, Application US/08652265
Patent No. 6025130
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Gnirke, Andreas
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
ITTLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Plopyy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: SMALCH, William M.
REGISTRATION NUMBER: 1957-000500
TELEPHONE: (415) 576-0300
TELEPHONE: (415) 576-0300
INFORMATION FOR INC. 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Prancisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               265 FQKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLPW 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
22; Mismatches
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LENGTH: 365 amino acids
TYPE: amino acid
Matches 210; Conservative
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NAMB/KEY: Protein

LOCATION: 1..365

OTHER INFORMATION:

US-08-652-265-23
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US-08-652-265-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 EWITGYAKANAQIDRVALRNILRRYNQSEAGSHILQGMNGCDMGPDGRLLRGYHQHAYDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 RADPRKAHVAHHPISDHEATLRCWALGPYPAEITLIWQRDGEEQTQDTELVETRPAGDGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 GSHSMRYFFTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQEGFEYW 84
                                                                                                                                                                                                                               1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 60
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                                                                                                                           Gaps
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APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gairke, Andreas
APPLICANT: Guirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchinashi, Zenta
APPLICANT: Wollf, Roger K.
TITLE OF INVENTION: HERBITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: AD
77.1%; Score 1154; DB 3; Length 365; 77.0%; Pred. No. 1e-104; Live 21; Mismatches 42; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTRY: New TOLK
COMPUTRY: New TOLK
COMPUTRY: USA
ZIP: 10036-2811
COMPUTRY: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
PRIOR APPLICATION STAP
FILING DATE: 16-APR-1996
CLASSIFICATION: 514
PRIOR APPLICATION STAP:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 04-APR-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
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ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERRICE/DOCKET NUMBER: 8907-0056-999
TELECOMMUNICATION INFORMATION:
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Patent No. 6140305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 KDYISLNEDLRSWTAADTVAQITQRFYBAEBYABBFRTYLEGECLELLRRYLENGKETLQ 180
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Patent No. 6153408
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Carcouge, Armanda
APPLICANT: Ashington
STREET: 1200
STREET: 1200
STREET: 1300 I Street, N.W., Suite 700
STREET: 12005-3315
COMPUTER: READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/370,476
FILING DATE:
CLASSIFICATION DATE:
PRIOR APPLICATION DATE:
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 77.1%; Score 1154; DB 3; Length 365; Best Local Similarity 77.0%; Pred. No. 1e-104; Matches 211; Conservative 21; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                /note= "Human Major Histocompatability
Class I (MHC) protein"
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TELEPHONE: 650-493-4935

TELERA: 661-493-5556

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
STRANDENNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
MAME/KEY: Protein
LOCATION: 1.365

OTHER INFORMATION: Class I ()
US-08-834-497A-23
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US-08-370-476-100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 77.1%; Score 1154; DB 3; Length 365; Best Local Similarity 76.6%; Pred. No. 1e-104; Matches 210; Conservative 22; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-00-503-444A-23
US-00-503-444A-23
US-00-503-444A-23
Sequence 23, Application US/09503444A
Patent No. 6228594
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Thomas, Winston J.
APPLICANT: Feder, John N.
APPLICANT: Freder, John N.
APPLICANT: Freder, John N.
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
ITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
SIRRFT.
PILING DATE: 07-52P-1993

PILING DATE: 07-52P-1993

APPLICATION NUMBER: US 08/072,787

FILING DATE: 06-JUN-1993

PRIOR APPLICATION NUMBER: US 07/801,818

APPLICATION NUMBER: US 07/801,818

FILING DATE: 05-DEC-1991

PRIOR APPLICATION DATA: US 07/792,473

APPLICATION NUMBER: US 07/792,473

ATTORNEY/AGENT INFORMATION:

NAME: MAYER: Xenneth J.

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 25,146

TELEPHONE: 202-408-4000

TELEPHONE: 202-408-4000

INPORMATION FOR SEQ ID NO: 100: SEQUENCE CHARACTERISTICS:

LENGTH: 365 amino acids
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STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 365 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECTLE TYPE: peptide
US-08-370-476-100
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120

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KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQ 180
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APPLICANT: Mottez, Estelle
APPLICANT: Abastado, dean-Pierre
APPLICANT: Abastado, dean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: Complex (MHC) Determinant and Methods for Using the
TITLE OF INVENTION: Determinant
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT
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CURRENT APPLICATION NUMBER: US/08/890,719A; CURRENT APPLICATION NUMBER: US/08/890,719A; CURRENT FILING DATE: 1997-07-09; EARLIER APPLICATION NUMBER: 60/021,685; EARLIER FILING DATE: 1996-07-10; NUMBER OF SEQ ID NOS: 39; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,905
FILING DATE: 07.-UNE-1995
CLASSIFTCATION TATA:
APPLICATION NUMBER: US/08/484,905
FILING DATE: 07.-UNME-1995
FILING DATE: 05.-DEC-1991
CLASSIFICATION: 530
CLASSIFICATION: 530
PILING DATE: 05.-DEC-1991
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                        77.1%; Score 1153; DB 3; 176.6%; Pred. No. 1.1e-104; ive 22; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 FOKWAAVVVPSGEEORYTCHVQHEGLPOPLILRW 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS-/MS-DOS
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Patent No. 5976551
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 76.6
Matches 210; Conservative
                                                                                                                                                                                                                                           LENGTH: 341
TYPE: PRT
CRGANISM: Homo sapiens
US-08-890-719-38
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Batent NO. 6075125
GENERAL INFORMATION:
APPLICANT: Bacon, Larry D
APPLICANT: Hunt, Henry D
APPLICANT: Hulton, Janet
TITLE OF INVENTION: Production of Antisera Specific to Major
TITLE OF INVENTION: Histocompatibility Complex Molecules in Chickens
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77.0%; Pred. No. 1e-104;
live 21; Mismatches 42;
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                                                                                                                                                                                                         PELGASIFLOATION:
PLEASIFLOATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 23 may-1996
FILING DATE: 3 may-1996
FILING DATE: 16-Apr-1996
FILING DATE: 16-Apr-1996
FILING DATE: 16-Apr-1996
FILING DATE: 16-Apr-1996
ATTORNEY AGENT INFORMATION:
NAME: POISSANT INFORMATION:
REGISTRATION NUMBER: 8907-0088-999
TELEPHONE: 212-790-990
TELEPHONE: 212-790-990
TELEPHONE: 212-790-990
TELEPHONE: 212-790-990
TELEPHONE: 212-790-990
TELEPHONE: 312-790-990
TELEPHONE: 312-790-990
TELEPHONE: 313-790-990
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TELEPHONE: 313-790-990
TELEPHONE: 313-790-990
TELEPHONE: 314-790-990
         CURRENT IBM PC compatible OPERATING SYSTEM: Windows 95 SOFTWARE: Wordferfect Version 8 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/503,444A FILING DATE: 14-Feb-2000 CLASSIFICATION: PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 365 amino acids
amino acid
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Best Local Similarity 77.05
Matches 211; Conservative
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OTHER INFORMATION:
OTHER INFORMATION:
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US-08-890-719-38
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APPLICATION NUMBER: US 07/792,473 FILING DATE: 15-NOV-1991

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TYPE: amino acid
TOPOLOGY: linear
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Determinant and Methods for Using the
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| Sequence 104, Application US/08484905
| Patent No. 597651
| GENERAL INFORMATION:
| APPLICANT: Mottez, Estelle
| APPLICANT: Kourilsky, Philippe
| TITLE OF INVENTION: Complex (MHC) Determinant and Methods
| TITLE OF INVENTION: Determinant and Methods
| TITLE OF INVENTION: Determinant and Methods
| TITLE OF INVENTION: Determinant of Methods
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,905
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 530
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                                                                                                                           REFERENCE/DOCKET NUMBER: 03495.0106-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 530
                                                                                                                                                                                                                          INFORMATION FOR SEQ 1D NO: 99: SEQUENCE CHARACTERISTICS: LENGTH: 365 amino acide TYPE: manno acid TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                  33,332
                         ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 76.3
Matches 209; Conservative
CLASSIFICATION:
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US-08-484-905-99
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Patent No. 6011146
GENERAL INFORMATION:
APPLICANT: Mottado, Jean-Pierre
APPLICANT: Kourilsky, Phillipe
TITLE OF INVERTION: Altered Major Histocompatibility Complex
TITLE OF INVERTION:
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match

76.9%; Score 1151; DB 2; Length 365;
Best Local Similarity 76.3%; Pred. No. 2e-104;
Matches 209; Conservative 22; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSE: Finnegan, Henderson, Farabow, Garrett & ADDRESSE: Finnegan, Henderson, Farabow, Garrett & ADDRESSE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
CITY: D.C.
ZIP: 20065-3315
COMPUTER REALBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,985B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRICR APPLICATION: 435
PRICR APPLICATION NUMBER: US 07/801,818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 FOXWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
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                                                                                                                                                                             03495.0106-03000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
                                        FILING DATE: 15-NOV-1991
CLASSIFICATION: 530
ATTORNEY AGENT INPORMATION:
NAME: POLICET, Jame E. R.
REGISTRATION NUMBER: 33,332
REPERSOMMINICATION INFORMATION:
TELEPHONE: 202-408-400
INFORMATION FOR SEG ID NO: 104: SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: peptide US-08-484-905-104
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SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
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Best Local Similarity 76.3
Matches 209; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear;
MOLECULE TYPE: peptide
US-08-481-9858-104
                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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Sequence 104, Application US/08481985B

Patent No. 601146

GENERAL INFORMATION:

APPLICANT: Mottez, Estelle

APPLICANT: Kourilsky, Phillipe

TITLE OF INVENTION: Altered Major Histocompatibility Complex

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 148

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dunner

STREET: 1300 I Street, N.W., Suite 700

CITY: Washington

STRATE: D.C.

TEN: 20005-3315
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CURRENT APPLICATION DATA:
CURLICATION NUMBER: US/08/481,985B
FILING DATE: 07-UN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 FOKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 274
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                                                                                                                                                                                                    03495.0106-04000
FILING DATE: 05-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                            ATTORNEY/AGENT INPORMATION:
NAME: MAYER: Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03499:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.9%;
                                                                                                                                                                                                                                                                                                                                : 365 amino acids
amino acid
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Best Local Similarity 76.3
Matches 209; Conservative
                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-481-985B-99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Lone, Yu-Chun
APPLICANT: Lone, Yu-Chun
APPLICANT: Officus, David
APPLICANT: Officus, David
APPLICANT: Officus, Lamanda
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Filmegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.9%; Score 1151; DB 3; Length 365; 76.3%; Pred. No. 2e-104; ive 22; Mismatches 43; Indels
                                                                                                                                                          FILING DATE: 15-NOV-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCYCES, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/POCKET NUMBER: 03495.0106-04000
TELECHONE: 202-408-400
TELECHONE: 202-408-4000
TELECHAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 104:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 FOXWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 435
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ZIP: 20005-3315
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
TYPE: TBM PC COMpatible
TYPE: TBM PC COMpatible
TYPE: TBM PC COMpatible
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Patent No. 6153408
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Sacuration No. 6153408

GENERAL INFORMATION:

APPLICANT: Mottles, Estelle

APPLICANT: Absatado, Jean-Pierre

APPLICANT: Lone, Yu-Chun

APPLICANT: Lone, Yu-Chun

APPLICANT: Casrouge, Armanda

TITLE OF INVENTION: Altered Major Histocompatibility Complex

TITLE OF INVENTION:

NUMBER OF ESQUENCES: 127

CORRESPONDENCE PADRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

ADDRESSEE: Dunner
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SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 FORWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
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                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,575
FILING DATE: 05-20N-1993
APPLICATION NUMBER: US 08/072,787
FILING DATE: 06-20N-1993
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
APPLICATION NUMBER: US 07/801,818
FILING DATE: 15-NOV-1991
APPLICATION NUMBER: US 07/92,473
FILING DATE: 15-NOV-1991
APPLICATION NUMBER: 25,146
REGISTRATION NUMBER: 25,146
REFENCE/DOCKET NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 25,146
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                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/370,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: peptide US-08-370-476-99
                                                                                                               FILING DATE
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61 EWTIGYAKANAQIDRVALRNILIRRYNQSEAGSHILQGMNGCDMGPDGRLLRGYHQHAYDG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 KDYISLNBDLRSWTAADTVAQITQRFYEAEEFAAEEFRTYLEGECLELLRRYLENGKETLQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 KDYIALKEDLRSWTAADMAAQTTKHKWEAAHVAEQWRAYLEGTCVEWLRRYLENGKETLQ 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 RIDAPKTHWTHHAVSDHEATLRCWALSFYPAEITLIWQRDGEDQTQDIELVETRPAGDGT 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 GSHSWRYFYTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRWBPRAPMIEQEGPEYW 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 76.9%; Score 1151; DB 3; Length 365; Best Local Similarity 76.3%; Pred. No. 2e-104; Matches 209; Conservative 22; Mismatches 43; Indels C
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Parent No. 5976551
GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05243.0001-01000
TELECOMMUNICATION INFORMATION:
TELEPRAN: 202-408-4400
INFORMATION FOR SEQ ID NO: 55QUENCE CHARACTERISTICS:
1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,575
FILING DATE: 06-UN-1933
APPLICATION NUMBER: US 08/072,787
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 15-NOV-1991
ATPONEY, AGENT INFORMATION:
NAME: MAYERS, KENDERH J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 365 amino acids
amino acid
                                                                          ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                         Washington
                                                                                                                                                                                                                                                                                                                                FILING DATE
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TITLE OF INVENTION: Complex(MAC) Determinant and Methods for Using the ITTLE OF INVENTION: Decembrant CORRESPONDENCE ADDRESS: 127
CORRESPONDENCE ADDRESS: 127
CORRESPEE: Intuner ADDRESS: 127
ADDRESSEE: Intuner ADDRESS: 127
ADDRESSEE: Intuner ADDRESS: 127
CORPUTER REALABLE FORM:
MEDIUM TYPE: 100 I Street, N.W., Suite 700
CITY: Weshington: N.W. Compatible COMPUTER: IN PAPLICATION DATA:
COMPUTER: IN PAPLICATION DATA:
MEDIUM TYPE: PAPLICATION DATA:
COMPUTER: PAPLICATION DATA:
MEDIUM TYPE: PAPLICATION DATA:
CLASSIFTACION: 300
FRIOR APPLICATION DATA:
PRINCE APPLICATION NUMBER: US 07/792,473
FILING DATE: 10-NOV-1991
FILING DATE: NOPERATION:
MANE: POETE: ADDRESS: 03495.0106-03000
TELESTAM: 20-408-400
INPERMINICATION INFORMATION:
TELESTAM: 20-408-400
INPERMINICATION INFORMATION:
TELESTAM: 20-408-400
INPERMINICATION TO SERVICE TREE: POETIGE
USED CONTRIBUTED T
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Search completed: June 18, 2004, 19:28:39 Job time : 23 secs

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June 18, 2004, 19:18:00 ; Search time 50 Seconds (without alignments) 1547.079 Million cell updates/sec
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1496
1 GSHSLRYFSTAVSRPGRGEP.....QRYTCHVQHEGLPQPLILRW 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Applications AA:*

1: /cgn2_6/prodata/2/pubpaa/USO7_PUBCOMB.pep:*

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18: /cgn2_6/prodata/2/pubpaa/USO0_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 5, Appli Sequence 82, Appl Sequence 4, Appli Sequence 4, Appli Sequence 1431, Ap Sequence 160, Appli Sequence 6, Appli Sequence 6, Appli Sequence 23, Appli Sequence 6, Appli
SUMMARIES	US-09-819-371-5 US-10-257-021-82 US-10-408-765A-1887 US-09-925-301-1431 US-10-10-380-880-7 US-10-210-17-160 US-10-210-17-160 US-10-093-463-78 US-10-093-463-80 US-10-138-888-23 US-10-138-888-23 US-10-138-888-23 US-10-073-300-6 US-10-073-300-5 US-10-075-257-5 US-10-075-257-5
DB	   1   1   1   2   1   1   1   1   1   1
* Query Match Length DB ID	
% Query Match	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Score	111 111 111 111 111 111 111 111 111 11
Result No.	

5511-5 5511-2 111-2 117-1156 1198-68 1198-68 1198-68 1198-70 1
12 US-10-108-511-5 12 US-10-108-511-2 13 US-10-065-10-172-156 15 US-10-065-108-72 15 US-10-065-108-78 15 US-10-138-108-70 12 US-10-138-108-70 13 US-10-138-58-32 14 US-10-138-58-32 14 US-10-015-535-24 14 US-10-015-535-34 14 US-10-015-535-34 14 US-10-015-535-34 14 US-10-015-535-34 15 US-10-015-535-34 16 US-10-015-535-34 17 US-10-015-535-34 18 US-10-015-535-34 19 US-10-015-535-34 10 US-10-015-535-34 115 US-10-015-535-34 12 US-10-015-535-34 13 US-10-015-535-34 14 US-10-015-535-34 15 US-10-015-535-34 17 US-10-015-535-34 18 US-10-015-535-34 19 US-00-08-10-10-10-10-10-10-10-10-10-10-10-10-10-
0 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
11153 77.1 11131.5 75.8 11131 75.6 11131 75.6 11131 75.6 1006 73.4 1006 71.3 1010 67.5 1010
116 1173 . 5 1173 . 5 10 10 10 10 10 10 10 10 10 10 10 10 10 1

## ALIGNMENTS

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Sequence 4, Application US/09819371
Publication No. US20040053344A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Using Thereof
TITLE OF INVENTION: Using Thereof
TITLE OF INVENTION: Using Thereof
TITLE OF SECTION NUMBER: US/09/819,371
CURRENT FILING DATE: 2002-03-15
CURRENT FILING DATE: 2002-03-15
SOGTWARE: Patentin version 3.0
SEQ ID NO 4
LEMIQTH: 362
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                           61 EWTTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT
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                                                                                                                                                                                                                                                                        Indels
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100.0%; Score 1496; DB 16;
Best Local Similarity 100.0%; Pred. No. 4.9e-140;
Matches 274; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
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NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1887
LENGTH: 442
                                                                                                                        TYPE: PRT
CORGANISM: Homo sapiens
US-10-408-765A-1887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EWITGYAKANAQTDRVALRNILRRYNQSEAGSHILQGMNGCDMGPDGRLLRGYHQHAYDG 120
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APPLICANT: Fahy, Eoin D.
APPLICANT: Tahy, Eoin D.
APPLICANT: Thang, Brad Gord W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Marnock, Dale B.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REPERENCE: 660089.465
CURRENT APPLICATION NUMBER: US/10/408,765A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                        APPLICANT: North, Patrice J.
APPLICANT: Sherman-Baust, Cheryl A.
APPLICANT: Sherman-Baust, Cheryl A.
APPLICANT: Hough, Colleen D.
TITLE OF INVENTION: TWORR MERKERS IN OVARIAN CANCER
FILE REFERENCE: 104014.0369U2.
CURRENT APPLICATION NUMBER: US/10/257,021
CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: 60/194,336
PRIOR APPLICATION NUMBER: 60/194,336
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 147
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 82
LENGTH: 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 1496; DB 12;
Best Local Similarity 100.0%; Pred. No. 3.8e-140;
Matches 274; Conservative 0; Mismatches 0;
                                                                                  241 FOKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FOXWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 295
                                                241 FOKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 274
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                                                                                                                                                                                                                   Sequence 82, Application US/10257021
Publication No. US20030211498A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CORGANISM: Homo sapiens
US-10-257-021-82
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US-10-408-765A-1887
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US-10-257-021-82
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APPLICANT: Stone, David
APPLICANT: Alsobrook II, John
APPLICANT: Lepley, Denise et al.
APPLICANT: Lepley, Denise et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHC
FILE REFERENCE: 21402-416 A
                                                                                                                                                                                                                                                                                                                  120
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                                                                                                                                                                                                                                             16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 RADPPKTHYTHHPVFDYBATLRCWALGFYPAEIILTWQRDGBDQTQDVBLVBTRPAGDGT
                                                                                                                                                                                                                                                                                                                      61 EWITGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG
                                                                                                                                                                               1 GSHSLRYFSTAVSRPGRGEPRYIAVBYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
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                                    Length 326;
                                                                                                         36; Indels
                                    79.1%; Score 1184; DB 12;
78.8%; Pred. No. 3.7e-109;
Live 22; Mismatches 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 160, Application US/10210172
Publication No. US20040043928A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Miller, Charles
APPLICANT: Pena, Carol
APPLICANT: Pena, Carol
APPLICANT: Rieger, Daniel
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PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/323, 994
PRIOR PILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/373, 814
PRIOR APPLICATION NUMBER: 60/310, 291
PRIOR APPLICATION NUMBER: 60/310, 291
PRIOR APPLICATION NUMBER: 60/310, 291
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Ji, Weizhen
Padigaru, Muralidhara
Casman, Stacie
Voss, Edward
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Hjalt, Tord
Rastelli, Luca
Spytek, Kimberly
Edinger, Shlomit
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Zerhusen, Bryan
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Anderson, David
Guo, Xiaojia
Zhong, Mei
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MacDougall, John
                                        Query Match
Best Local Similarity 78.8%
Matches 216; Conservative
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Gorman, Linda
Leite, Mario
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Publication No. US20040044182A1

GENERAL INFORMATION:

APPLICANT HURL, JOAN S.

APPLICANT HURL, JOAN S.

TITLE OF INVENTION:

TITLE OF INVENTION: US20040044182A1 30772

FILE REFERENCE: Docket No. US20040044182A1 30772

FILE REFERENCE: Docket No. US20040044182A1 30772

FILE REPRENCE: Docket No. US2
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APPLICAMT ROSSEL et al.

IIILE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAJO6

CURRENT APPLICATION NUMBER: US/09/925,301

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05882

PRIOR FILING DATE: 1990-03-12

NUMBER: OF SEQ ID NOS: 1694

SOFTWARE: PATENTIN UVER: 2.0

SEQ ID NO 1431

LENGTH: 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.6%; Score 1311; DB 9; Length 271;
99.6%; Pred. No. 6.5e-122;
.ive 1; Mismatches 0; Indels
262 FQKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 295
                                                                                                                                                                                                            ; Sequence 1431, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.6
Matches 241; Conservative
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US-09-925-301-1431
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CRGANISM: Homo sapiens
US-10-380-880-7
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FR 269
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US-10-380-880-7
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Spaderna, Steven
Voss, Edward
Malyankar, Uriel
Anderson, David
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US-10-093-463-78
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Best Local Similarity
Matches 216; Conservat
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       PRIOR FILING DATE: 2001-08-08

PRIOR PILING DATE: 2001-08-08

PRIOR PILING DATE: 2001-08-07

PRIOR PELING DATE: 2001-08-07

PRIOR PELING DATE: 2001-08-07

PRIOR PELING DATE: 2001-08-07

PRIOR PELING DATE: 2001-08-17

PRIOR PELING DATE: 2001-08-13

PRIOR PELING DATE: 2001-08-17

PRIOR PELING DATE: 2001-08-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEO ID NOS: 327

SOFTWARE: CuraSequist version 0.1

SEQ ID NO 160

LENGTH: 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Gaps
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78.5%; Score 1174.5; DB 12; Length 379;
Best Local Similarity 78.0%; Pred. No. 4e-108;
Matches 216; Conservative 22; Mismatches 36; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 DGTFQKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 274
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APPLICATION NUMBER: 60/310,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 78, Application US/10093463 Publication No. US20030208039A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Badigaru, Muralidhara
APPLICANT: Shenoy, Suresh
APPLICANT: Kekuda, Ramesh
APPLICANT: Glusev, Vladimir
APPLICANT: Pochart, Pascal
APPLICANT: Zhong, Mei
APPLICANT: Rastelli, Luca
APPLICANT: Rastelli, Luca
APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: Guo, Xiaojia
APPLICANT: Granan, Stacie
APPLICANT: Granan, Stacie
APPLICANT: Bolddy, Ferenc
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Tchernev, Velizar
Gangolli, Esha
Vernet, Corine
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Liu, Xiaohong
Spytek, Kimberly
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
US-10-210-172-160
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Pena, Carol
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APPLICANT:
APPLICANT:
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PRPLICANT: Anderson, David
APPLICANT: Anderson, David
APPLICANT: Miller, Charles
APPLICANT: Miller, Charles
APPLICANT: Taugher, Charles
APPLICANT: Taugher, Charles
APPLICANT: Taugher, Charles
APPLICANT: Taugher, Raymond
ITTLE OF INVEXTION: No. U52003203031e1 Antibodies that Bind to Antigenic Polypep
ITTLE OF INVEXTION: Broading The Antigens, and Methods of Use.
ITTLE OF INVEXTION: Broading The Antigens, and Methods of Use.
CURRENT PAPLICATION NUMBER: 12002-06-207
PRIOR FILING DATE: 2001-04-14
PRIOR PLING DATE: 2001-04-14
PRIOR PLING DATE: 2001-04-14
PRIOR PLING DATE: 2001-03-06
PRIOR APPLICATION NUMBER: 6001-03-06
PRIOR APPLICATION NUMBER: 6001-03-03
PRIOR APPLICATION NUMBER: 6001-03-03
PRIOR APPLICATION NUMBER: 6001-03-03
PRIOR APPLICATION NUMBER: 6001-03-03
PRIOR APPLICATION NUMBER: 6001-03-03-03
PRIOR APPLICATI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 YDGKDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 BEETRNIKAHAQIDRMNLQILRGYYNQSEGVGPGSHTLQWMIGCDLGSDGRLLRGYEQYA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 GSHSWRYFSAAVSRPGRGEPRFIAMGYVDDTQFVRFDSDSACPRWEPRAPWVEQEGPEYW 84
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llarity 78.0%; Pred. No. 4e-108;
Conservative 22; Mismatches 36; Indels
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APPLICANT: Spycek Kimberly
APPLICANT: Gorman, Linder
APPLICANT: Gorman, Linder
APPLICANT: Gorman, Linder
APPLICANT: Godenman, Steven
APPLICANT: Godenman, Steven
APPLICANT: Godenman, Steven
APPLICANT: Godenman, Steven
APPLICANT: Malystadar: Unia
APPLICANT: APPLICANT: S002-06-24
REING APPLICANT: S003-06-24
REING APPLICANT: WINDER: 60/230, 091
REING APPLICANT: WINDER: 60/230, 661
REING APPLICANT: WINDER: 60/230, 661
REING APPLICANT: WINDER: 60/230, 661
REING APPLICANT: WINDER: 60/230, 692
REING APPLICANT: WINDER: 60/230, 693
REING APPLICANT: WINDER: 60/230, 993
REING APPLICANT: 900-69-69
REI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 EWTŢĠŶĄKANĄQTDŖVAĻŖNĮĻŖRŶŊQSĘĄĠŚĦŢĹQĠMNĠĊĎMĠPĎĠŖĹĹŖĠŶĤQĤĄŶĎĠ
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                          Liu, Xiaohong
Spytek, Kimberly
Gorman, Linda
Spaderna, Steven
Voss, Edward
Malyankar, Uriel
Anderson, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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Publication No. US20040053344A1

GENERAL INFORMATION:

TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Cantille Represence: 30815

TITLE OF INVENTION: Using Thereof

FILE REPRESENCE: 30815

CURRENT APPLICATION NUMBER: US/09/819,371

CURRENT PILING DATE: 2002-03-15

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin version 3.0
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178 TLORADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWORDGEEQTODTELVETRPAG 237
                                   205 MLQRADPPKTHVTHHPVFDYBATLRCWALGFYPABIILTWQRDGBDQTQDVBLVBTRPAG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 RRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDGKDYISLNEDLRSWTAADTVAQI 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQRADPPKAHVAHHPISDHEATLR 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 IAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYWEWTTGYAKANAQTDRVALRNIL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYWEWTTGYAKANAQTDRVALRNLL
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                                                                                                           238 DGTFOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
                                                                                                                                            265 DGTFQKWAAVVVPSGEEQRYTCHVQHEGLPEPLMLRW 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CWALGFYPAEITLTWQRDGEEQTQDTELVETRPAG 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Padigaru, Muralidhara
APPLICANT: Shenoy, Suresh
APPLICANT: Kekuda, Rameeh
APPLICANT: Reaclad, Rameeh
APPLICANT: Pochart, Pascal
APPLICANT: Rastelli, Luca
APPLICANT: Rastelli, Luca
APPLICANT: Rastelli, Luca
APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Stacie
APPLICANT: Casman, Stacie
APPLICANT: Boldoy, Ferenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zerhusen, Bryan
Tchernev, Velizar
Gangolli, Esha
Vernet, Corine
Pena, Carol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.5'
Matches 214; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
US-09-819-371-6
                                                                                                                                                                                                                                                     RESULT 9
US-09-819-371-6
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Gaps

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Sequence 6, Application US/10073300
Publication No. US20030003535A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICATY: Reliter, Yoram
TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO- COMPATIBILITY COMPLEXES
CURRENT APPLICATION WINBER: US/10/073,300
CURRENT FILING DATE: 2002-06-25
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.0
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 280
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KDYISLNEDLRSWTAADTVAQITORFYEAEBYAEBFRTYLEGECLELLRRYLENGKETLQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EWITGYAKANAQIDRVALRNILRRYNQSEAGSHTLQGWNGCDMGPDGRLLRGYHQHAYDG 120
                                                                                                                                                             61 EWTTGYAKANAQTDRVALRNILRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 120
                                                                                                                                                                                                85 DGETRKVKAHSQTHRVDLGTLRGYYNQSEAGSHTLQNMFGCDVGSDWRFLRGYHQYAYDG 144
                                                                                                                                                                                                                                                                                                                             181 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLIWQRDGEEQTQDTELVETRPAGDGT 240
                                                                                                                                                                                                                                              121 KDYISLNEDLRSWIAADIVAQIIQRFYEAEEFRIYLEGECLELLRRYLENGKEILQ 180
                                                                                                                                                                                                                                                                        121 KDYIALKEDLRSWTAADMAAQTTKHKWEAAHVAEQLRAYLBGTCVEWLRRYLENGKETLO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRWEPREPWVEQEGPQYW
                                                                                                      25 GSHSMRYFFTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQEGPEYW
                                                                                1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
    Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 280;
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                                           Indels
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76.6%; Pred. No. 3.6e-106;
iive 22; Mismatches 42;
Query Match 77.1%; Score 1154; DB 14; Best Local Similarity 77.0%; Pred. No. 4.1e-106; Matches 21; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                            265 FQKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLRW 298
                                                                                                                                                                                                                                                                                                                                                                                                                241 FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 6, Application US/10075257; Publication No. US20040086960A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 77.1%
Best Local Similarity 76.6%
Matches 210; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-10-073-300-6
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US-10-075-257-6
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      145 KDYIALNEDLHSWTAANTAAQISQHKWEADKYSEQVRAYLEGKCMEWLRRHLENGKETLQ 204
                                                                   RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWORDGEEQTODTELVETRPAGDGT 240
                                                                                                  205 HADPPKAHVTQHPISDHEATLRCWALGLYPAEITLFWQQDGEDQTQDTELVETRPAGDGT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Human Major Histocompatability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTAT: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                   241 FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Brian M. Poissant
REGISTATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFRAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/634,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/622,265
FILING DATE: 12-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Hereditary Hemochrom:
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1..365
OTHER INPORMATION: /note= "
Class I (MHC) protein"
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 365 amino acids
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TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/10073300

Publication No. US2033003535A1

GENERAL INFORMATION:

APPLICANT Reiter, Yoram

TILE OF INVENTON: SINGLE CHAIN CLASS I MAJOR HISTO- COMPATIBILITY COMPLEXES

TILE REFERENCE: 02/23339

CURRENT APPLICATION UNMBER: US/10/073,300

CURRENT PILING DATE: 2002-06-25

NUMBER OF SEQ ID NOS: 2002-06-25

SEQ ID NO 5

LENGTH: 415
APPLICANT: Reiter, Yoram
TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO-COMPATIBILITY COMPLEXES,
TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO-COMPATIBILITY COMPLEXES,
TITLE OF INVENTION: CONSTRUCTS ENCODING SAME AND METHODS OF GENERATING SAME
FILE REFERENCE: 02/23338
CURRENT APPLICATION NUMBER: US/10/075,287
CURRENT FILING DATE: 202-02-15
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PALENT NESSOR NOS: 20
LENGTH: 280
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                                                                                                                                                                                                                           77.1%; Score 1153; DB 16; Length 280; 76.6%; Pred. No. 3.6e-106; ive 22; Mismatches 42; Indels 0;
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ORGANISM: Artificial Sequence
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Best Local Similarity 76.6%
Matches 210; Conservative
                                                                                                                                                                                                                              Query Match
Best Local Similarity 76.61
Matches 210; Conservative
                                                                                                                                                                TYPE: PRT
CORGANISM: Homo sapiens
US-10-075-257-6
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US-10-073-300-5
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RESULT 15
US-10-075-257-5
i Sequence 5, Application US/10075257
j Sequence 5, Application US/20040086960A1
j GENERAL INFORMATION:
APPLICANT: Reiter, Yoram
APPLICANT: Reiter, Yoram
TITLE OF INVENTION: SINGELE CHAIN CLASS I MAJOR HISTO-COMPATIBILITY COMPLEXES,
TITLE OF INVENTION: CONSTRUCTS ENCODING SAME AND METHODS OF GENERALING SAME
ILLE REFERENCE: 02/23338
CURRENT FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 415
LENGTH: 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: Human beta2 microglobulin linked to MHC class I heavy chain US-10-075-257-5
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236 KDYIALKEDLRSWTAADMAAQTTKHKWEAAHVAEQLRAYLEGTCVEWLRRYLENGKETLQ 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 KDYISLNEDLRSWTAADTVAQITQRFYEAEBYAEBFRTYLEGECLELLRRYLENGKETLQ
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                                                                        1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREFWVEQEGPQYW
                                               RADPPKAHVAHHPISDHEATLRCWALGFYPABITLTWORDGBEOTODTELVETRPAGDGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
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                                                                                                                                                        356 FQKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLRW 389
                                                                                                                                 241 FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
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Job time : 52 secs
                                                    181
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

June 18, 2004, 19:19:06; Search time 18 Seconds (without alignments) 792.623 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-819-371-5 1496 1 GSHSLRYFSTAVSRPGRGEP......QRYTCHVQHEGLPQPLILRW 274

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

141681 seqs, 52070155 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMEDIES

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## ALIGNMENTS

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FUNCTION: Involved in the presentation of foreign antigens to the
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InterPro; IPR003597; Ig-like.
InterPro; IPR003597; Ig-cl.
InterPro; IPR003597; Ig-cl.
InterPro; IPR001039; MFC_I.
Finan; Pr00129; MFC_I.
Pfam; Pr00129; MFC_I.
PRINTS; PR00129; MFC_I.
PROSITE; PS0029; IG-Like; I.
PROSITE; PS00290; IG-Like; I.
PROSITE; PS00290; IG-MFC; I.
                                                                                                                                                                                           EMBL; M30685; AAA87973.1; -.
HSSP; Q30201; 1A6Z.
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98.5%;
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Best Local Similarity 98.5
Matches 270; Conservative
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346 AA;
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                                                                                                                                                                                                                                                                                                                                                                          Gaps
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01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CHLA class I histocompalibility antigen, CH28 alpha chain precursor.
Pan troglodytes (Chimpanzee).
Bukaryota, Metazoa, Chordata, Craniata; Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates; Catarrhini; Hominidae, Pan.
NCBI_TAXID=9598;
                                                                                                                                                                                                                                                    CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (BY SIMILARITY).
BBDD041F820A34E1 CRC64;
                                                                                                                                                    CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINES 88319000; PubMed=1412487; MEDLINES 88319000; PubMed=1412487; Lawlor D.A., Ward F.E., Ennis P.D., Jackson A.P., Parham P.; "HLA-A and B polymorphisms predate the divergence of humans and
                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                             DB 1; Length 362;
                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-2.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1496; DB 1
100.0%; Pred. No. 4e-113;
tive 0; Mismatches 0
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InterPro; IPR001039; MHC_I.
Pfam; PF001047; ig; 1.
Pfam; PF001047; ig; 1.
Pr01029; MHC_I. 1.
PR01039; MHC_I. 1.
PR00000; PD000050; MHC_I; 1.
SMART; SM00407; IGC,I. 1.
PROSITE; PS00230; IG_MHC,I. 1.
PROSITE; PS00230; IG_MHC, 1.
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                                                                                                                                                                                                                                                                                                                 40568 MW;
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Nature 335:268-271(1988)
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122
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362 AA;
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Best Local Similarity
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1C28 PANTR
ID 1C28 PANTR
AC P16215;
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 KDYISLNEDLRSWTAADTVAQITQRFYEAEEFAEBFRTYLEGECLELLRRYLENGKETLQ 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 EXTRACELULAR ALPHA-1.
203 EXTRACELULAR ALPHA-2.
295 EXTRACELULAR ALPHA-2.
305 CONNECTING PEPTIDE.
329 CYTOPLASMIC TAIL.
185 BY SIMILARITY.
280 BY SIMILARITY.
107 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
A; 39084 MW; F83E882D5C2E0971 CRC64;
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
immune system.
-1- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).
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Pred. No. 3.8e-111;
1; Mismatches 3; Indels (
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(Rel. 28, Last sequence update)
(Rel. 38, Last annotation update)
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HLAF MACUU
1D HLAF MACMU
AC P33617;
DT 01-FEB-1994 (
DT 15-JUL-1999 (
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202 LORADPPKAHLAHHPVSDREATLRCWALGFYPDEITLTWQRDGEEQTQDTELVETRPAGD 261
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LORADPPKAHVAHHPISDHEATLRCWALGPYPAEITLTWQRDGEEQTQDTELVETRPAGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEQUENCE OF 25-361 FROM N.A. (B*2701).
MEDLINE=86149317; PubMed=3485286;
Szocts H., Riethmu-ller G., Weiss E., Meo T.;
"Complete sequence of HLA-B27 cDNA identified through the characterization of structural markers unique to the HLA-A, -B, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (B*2701 AND B*2702).
MEDLINE=86220133; PubMed=3011411;
Seemann G.H.A., Rein R.S., Brown C.S., Ploegh H.L.;
"Gene conversion-like mechanisms may generate polymorphism in human class I genes.";
EMBO J. 5:547-552(1986).
                                                                                                                                                                                                                                                                                                                                                                                                  23-0CT-1986 (Rel. 02, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
HIA class I histocompatibility antigen, B-27 alpha chain precursor (MHC class I antigen B*27).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    structure of papain-solubilized human histocompatibility
                                                                                                                                                                                                                                                                                                                   1B27 HUMAN STANDARD; PRT; 362 AA.
P03989; P10317; P10318; P19373; P30467; Q08136; Q29693; Q29846;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=85226361; PubMed=2408663; Ezquerra A., Brago R., Vega M.A., Strominger J.L., Woody J., Lopez de Castro J.A.;
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Moses J.H., Marsh S.G.E., Arnett K.L., Adams E.J., Bodmer J.G.
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MEDLINE=86138405; PubMed=3912316;
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Tissue Antigens 46:50-53(1995).
                                                                                                                                               262 GIFQKWAAVVVPSGEEQRYTCHVQHEGLPQPLILLRW 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -C allelic series.";
Proc. Natl. Acad. Sci. U.S.A. 83:1428-1432(1986)
                                                                                                                239 GIFOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 86-107 AND 171-181 (B*2702).
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MEDLINE=88227491; PubMed=3286582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigen HLA-B27.";
Biochemistry 24:1733-1741(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenetics 38:141-145(1993).
-!- FUNCTION: Involved in the presentation of foreign antigens to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune system.
-!- SUBUNIT: Hererodimer of an alpha chain and a beta chain (beta-2-microglobulin).
      class I histocompatibility antigen, alpha chain F precursor (HLA
                                                                                                                                                                                                                                                                                                                         Otting N., Bontrop R.E.; "Characterization of the rhesus macaque (Macaca mulatta) equivalent
                                                                                     Macaca mulatta (Rhesus macaque).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
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4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                          MEDLINE=93246295; PubMed=8482576;
                              antigen) (Leukocyte antigen F)
HLA-F OR HLAF.
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                                                                                                                                                                             Cercopithecinae; Macaca.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                           NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                   of HLA-F."
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Hulsmeyer M., Hillig R.C., Volz A., Ruhl M., Schroder W., Saenger W.,
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Rognan D., Scapozza L., Folkers G., Daser A.;
"Rational design of nonnatural peptides as high-affinity ligands for the HLA-B*2705 human leukocyte antigen.";
Proc. Natl. Acad. Sci. US.A. 92:753-757 (1995).
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SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
Choo S.Y., St John T., Orr H.T., Hansen J.A.;
"Molecular analysis of the variant alloantigen HLA-B27d (HLA-B*2703)
identifies a unique single amino acid substitution.";
Hum. Immunol. 21:209-219(1998).
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Madden D.R., Gorga J.C., Strominger J.L., Wiley D.C.;
"The structure of HLA-B27 reveals nonamer self-peptides bound in settended conformation.";
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Madden D.R., Gorga J.C., Strominger J.L., Wiley D.C.;
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"The HLA-B7Qui antigen is encoded by a new subtype of HLA-B27
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                                                                                                                                                                                                                                                    MEDLINE=94102824; PubMed=8276469; Vilches C., de Pablo R., Kreislar M.; "Nucleotide sequence of HLA-B*27065"; Immunogenetics 39:219-219(1994).
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Tissue Antigens 44:47-51(1994).
                                                                                                                                                                                              [mmunogenetics 43:160-162(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (B*2709).
                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (B*2706)
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (B*2707)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (B*2708)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 353:321-325(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rissum=Blood;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its way mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- POLYMORPHISM: The following alleles of B-27 are known:
B*2701_B*2705, B*2702 (B27.2; B-27k; B27e), B*2703 (B27d), B*2704,
B*2704_B*2707, B*2708 (B7Qui) and B*2709 (B27-ci). The sequence shown is that of B*2701.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein; Signal; Polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B-27 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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| InterPro; | IPR003597; | Ig cl. |
| InterPro; | IPR003597; | Ig cl. |
| InterPro; | IPR001006; | Ig MHC |
| InterPro; | IPR001039; | MHC |
| Pfam; | PF00129; | MHC | I. |
| PRNITS; | PF00129; | MHC | I. |
| PRNITS; | PF00129; | MHC | I. |
| PRNITS; | PF00129; | MHC | I. |
| PROSITE; | PF00129; | IG LIKE; | I. |
| PROSITE; | PS00290; | IG LIKE; | I. |
| PROSITE; | PS00290; | IG LIKE; | I. |
| PROSITE; | PS00290; | IG LIKE; | I. |
| Destructure. |
| I Transmembrane; | Glycoprote |
| I Transmembrane; | Glyco
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CAA27302.1)
AAA3622.1.1)
AAC50444.1)
AAC50447.1)
CAA51380.1)
AAA59688.1)
CAA53688.1)
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L38504; AAA69724.1;
M54883; AAA59616.1;
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PIR, 156116; 156116.

PIR, 1804; 30-8EP-94.

PIR, 1804; 30-8EP-94.

PIR, 1804; 30-8EP-94.

PIR, 30-8EP-94.
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2298
3398
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U35734; 1
X73578; 0
M62852; 1
L19923; 1
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M12967;
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333
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227
110
362 AA;
DOMAIN
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DISULPID
CARBOHYD
SEQUENCE
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                                                      180
                                                                                              240
                                                                                                                    264
             120
                           204
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=92078860; PubMed=1744581;
Lawlor D.A., Warren B., Taylor P., Parham P.;
Lawlor J.A., Warren B. Taylor P., Parham P.;
Gorilla class I major histocompatibility complex alleles: comparison to human and chimpanzee class I.";
J. Exp. Med. 174:1491-1509(1991).
-:- FUNCTION: Involved in the presentation of foreign antigens to the
             EWTTGYAKANAOTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG
                                                      KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQ
                                                                 181 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLITWQRDGEEQTQDTELVETRPAGDGT
                                                                                                                   RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTELVETRPAGDRT
                                                                                                                                                                                                                                     01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
Class I histocompatibility antigen, GOGO-B0103 alpha chain precursor.
Gorilla gorilla (Lowland gorilla)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Craniati; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                        immune system.
-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diyoprotein, Signal.

4 Elysoprotein, Signal.

2 CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0103 ALPHA-CHAIN.

4 EXTRACELLULAR ALPHA-1.

6 EXTRACELLULAR ALPHA-2.

8 CONNECTING PEPTIDE.
                                                                                                                                         274
                                                                                                                                                    265 FQKWAAVVVPSGEBQRYTCHVQHEGLPKPLTLRW 298
                                                                                                                                         POKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW
                                                                                                                                                                                                                 362 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00147; ig; 1.
Pfam; PF00129; MHC I.1
PRINTS; PR0129; MHC I.1.
ProDom; PF000050; MHC I.1.
ProDom; PF000050; MHC I; I.
PROSITE; PS00250; IG LIK; I.
PROSITE; PS00290; IG LIK; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR, JH0541; JH0541.
HSSP; P03989; 1HSA.
INCERPRO; IPR007110; Ig-like.
INCERPRO; IPR003597; Ig_C1.
INCERPRO; IPR003006; Ig_MHC.
INCERPRO; IPR001039; MHC_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X60254; CAA42806.1; -.
                                                                                                                                                                                                                   STANDARD;
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206
208
308
332
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1115
207
209
309
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P30381;
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DOMAIN
TRANSMEM
                                                                           145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RADPPKAHVAHHPISDHEATLRCWALGFYPABITLTWQRDGEEQTQDTELVETRPAGDGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (B*3904).

TISSUB=Peripheral blood;

MEDLINE=95189597; BubMed=7533753;

Ogwan A., Tokunaga K., Nakajima F., Kikuchi A., Karaki S.,

Kashiwase K., Ge J., Hannestad K., Juji T., Takiguchi M.;

"Identification of the gene encoding a novel HLA-B39 subtype. Two
amino acid substitutions on the beta-sheet out of the peptide-binding
floor form a novel serological epitope.";

Hum. Immunol. 41:241-247(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 EWTTGYAKANAQTDRVALRNILIRRYNQSEAGSHTLQGMNGCDMGPDGRLIRGYHQHAYDG
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of
                                                   BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (BY SIMILARITY).
3DEB82572BD81469 CRC64;
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P30475; 002960; 078217; P30476; P79504; 029665; 029697; 029749; 029847; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 029852; 0
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MEDLINE=93131294; PubMed=8420828;
Kato N., Karaki S., Kashiwase K., Mueller C., Akaza T., Juji
Kano K., Takiguchi M.;
"Molecular analysis of HLA-B39 subtypes.";
Immunogenetics 37:212-216(1993).
                                                                                                                                                                                                                                                                                         Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "HLA-B16 antigens: sequence of the ST-16 antigen, further of two B38 subtypes and evidence for convergent evolution (B*3902.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (B*3902 AND B*3905).
MEDLINE=95242308; PubMed=7725307;
MEDLINE=95242308; Arnett K.L., Little A.-M.,
Adams B.J., Martinae.Naves B., Arnett K.L., Little A.-M.,
Tyan D.B., Parham P.;
"ḤLA-B16 antigens: sequence of the ST-16 antigen, further
                                                                                                                                                                                                                                                                                                                                                                                     33; Indels
                                                                                                                                                                                                                                                                                              82.1%; Score 1228; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 FOKWAAVVVPSGEEORYTCHVQHEGLPOPLILRW 274
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CYTOPLASMIC TAIL
                                                                                                                                                                                                                                                                                                                                                                                          16; Mismatches
                                                                                                                                                                                                                                                                                                                                            Pred. No.
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                                                                                                                                                                                                  40248 MW;
                                                                                                                                                                                                                                                                                                                                                 82.1%;
                                                                                                                                                                                                                                                                                                                                            Local Similarity 82.1 hes 225; Conservative
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Ramos M., Postigo J.M., Vilches C., Layrisse Z., Lopez de Castro J.A.; Primary structure of a novel HLA-B39 allele (B*3909) from the Warao Indians of Venezuela. Further evidence for local HLA-B diversification in South America."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [10]
SEQUENCE FROM N.A. (B*3924).
SEQUENCE PERIPHERAL DIOOG,
TISSUE=Peripheral blood,
TISSUE=Peripheral blood,
TISSUE=Peripheral blood,
TISSUE=Peripheral blood,
Estefania E., Gomez-Lozano N., de Pablo R., Moreno M.E., Vilches C.,
"Complementary DNA sequence of the HLA-B*3924 allele.";
Eur. J. Immunogenet. 30:11-12(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE PROM N.A. (B*3910).
MICHIGHE 97378891; PubMed=9234488;
Vilches C., Bunce M., de Pablo R., Moreno M.E., Puente S., Sanz L.,
Kreisler M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The novel HLA-Cw*1802 allele is associated with B*5703 in the Bubi population from Equatorial Guinea.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 10-362 FROM N.A. (B*3908).
MEDLINE=96435470; PubMed=8838356;
Adams E.J., Little A.-M., Arnett K.L., McAuley J.E., Williams R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20066996; Pubmed=1060013;
Lazaro A.M., Moraes M.E., Marcos C.Y., Moraes J.R.,
Fernandez-Vina M.A., Stastny P.;
"Evolution of HiA-class I compared to HiA-class II polymorphism in
"Evena, a South-American Indian tribe.";
Hum. Immunol. 60:1138-1149(1999).
                                                                                                                                                                                       Fernandez-Vina M.A., Lazaro A.M., Araujo H.A., Miller S.,
                                                                                                                                                                                                                                                                                                                                                                                         Wells R.S., Parham P.; "A novel recombinant HLA-B*39 allele (B*3910) in a South African
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 26-206 FROM N.A. (B*3923).
MEDLINE=21160452; PubMed=11260515;
Akebaka T., Kashiwase K., Ishikawa Y., Tanaka H., Shimizu M.,
Kawai S., Akaza T., Takahashi T., Juji T.;
"Allele frequency of HLA-B39 in the Japanese population and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 26-206 FROM N.A. (B*3912).
MEDLINE=9929758; PubMed=10372543;
Marcos C.Y., Fernandez-Vina M.A., Lazaro A.M., Moraes M.E.,
Moraes J.R., Stastny P.;
"Novel HiA-A and HiA-B alleles in South American Indians.";
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (B*3906).
Zhang L., Ellexson M.E., Hildebrand W.H.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kashiwase K.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Three new HLA-B alleles found in Mexican-Americans.";
                                                                                                                                                                                                                           "Full cDNA of a novel HLA-B39 subtype, B*39061.";
Tissue Antigens 47:435-437(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 26-206 FROM N.A. (B*3912).
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                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (B*3910),
MEDLINE=97142356; PubMed=8988545;
                                                                                                                                                                                                                                                                                                                                                                                                                                            issue Antigens 48:595-597(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue Antigens 46:414-416(1995).
                 TISSUE=Blood;
MEDLINE=96435466; PubMed=8838352;
                                                                                                                                                                           MEDLINE=96387677; PubMed=8795147;
                                                                                                                     Tissue Antigens 46:401-404(1995)
                                                                                                                                                         SEQUENCE FROM N.A. (B*3906).
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SEQUENCE FROM N.A. (B*3909).
                                                                                                                                                                                            Zhao W., Fe:
Stastny P.;
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                                                   SECURNCE OF 60-196 FROM N.A. (B*3907).
MEDLINE=95317819; PubMed=7797264;
Garber T.L., Butler L.M., Trachtenberg E.A., Erlich H.A., Rickards O.,
De Stefano G., Watkins D.I.;
HLA-B alleles of the Cayaga of Ecuador: new B39 and B15 alleles.";
Immunogenetics 42:19-27(1995).
                                                                                                                                                                        -! - FUNCTION: Involved in the presentation of foreign antigens to the
                                                                                                                                                                                                                                  microglobulin).
-:- SUBCELLULAR LOCATION: Type I membrane protein.
-:- POLYMORPHISM: The following allels of B-39 are known: B*3901
-:- POLYMORPHISM: The following allels of B-39 are known: B*3901
(B39.1), B*3902 (B9.2), B*3907 (B39404), B*3910, B*3912 (B3901v),
B*3906 (B396), B*3907 (B39404), B*3909, B*3910, B*3912 (B3901v),
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                                                                                                                                                                                                   immune system.
-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein, Signal; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A GO; GO:0005887; C:integral to plasma membrane; NAS.

GO; GO:000305; F:MHC class I receptor activity; NAS.

GO; GO:000395; P:immune response; NAS.

InterPro; IPR00710; Ig-11ke.

R InterPro; IPR0010597; Ig-01.

R InterPro; IPR001039; MHC.

R InterPro; IPR001039; MHC.

R Pfan; PP001029; MHC.

R PFAn; PP001029; MHC.

R ProDom; PD000050; MHC.

R ProDom; P000050; MHC.

R PROSITE; PS00385; IG-11.

R PROSITE; PS00385; IG-11.
identification of a novel B39 allele, B*3923.";
Tissue Antigens 57:169-172(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U76395; AAB39108.1; -.
U76394; AAB39108.1; JOINED.
AB032097; BAA84116.1; -.
U15640; AAA74047.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BAC11810.1; -.
BAC11811.1; -.
AAN63555.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M94052; AAA566811; EMBL; M94051; AAA56601; EMBL; M94053; AAA56601; EMBL; U04243; AAA596501; EMBL; L22649; AAA79421; EMBL; L22649; AAA79421; EMBL; L42024; AAB54841; EMBL; U29083; AAC327411; EMBL; U52646; AAB54841; EMBL; U52646; AAB54841; EMBL; U52646; AAB54811; EMBL; U52646; AAB54811; EMBL; V99058; CAA702611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AB091218; BAC11811.1; -
AF428252; AAN63555.1; -
L42280; AAB51452.1; -
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EMBL; U76395; AAB3108
EMBL; U76395; AAB3108
EMBL; AB032097; BAA641
EMBL; U15640; AAA74047
PIR; I38876; I38876.
PIR; I54314; I54314.
PIR; I54865; I68850.
PIR; I84488; I84488.
HSSP; P30460; IAGD.
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EMBL;
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DOMAIN
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CARBOHYD
DISULFID
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EWITGYAKANAQIDRVALRNILLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                          SS DRNTQICKTNTQTDRESLRNLRGYYNGSEAGSHTLQRMYGCDVGPDGRLLRGHNQFAYDG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTODTELVETRPAGDGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RADPPKTHYVTHHPISDHEATLRCWALGFYPAEITLTWQRDGBDQTQDTELVETRPAGDRT 264
                                                                                                                                                                                                                                                                                                                                                 90
                                                                                                                                                                                                                                                                                                                                                                   25 GSHSMRYFYTSVSRPGRGEPRFISVGYVDDTQFVRFDSDAASPREEPRAPWIEQEGFEYW 84
                                                                                                                                                                                                                                                                                                                                                 1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
                                                                                                                                                                                                                                                                                                             Gaps
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MEDLINE-94294981; Pubmed-7517584;
MIDLINE-94294981; Pubmena J.D., Hildebrand W.H., Shen S.Y., Barber L.D., Marsh S.G.E., Bias W.B., Parham P.;
"HiA-B67: a member of the HIA-B16 family that expresses the ME1
                                                                                      N-LINKED (GLCNAC. . .) (BY SIMILARITY).
BY SIMILARITY.
Y -> D (in allele become.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1867 HUMAN STANDARD, PRT, 362 AA.

(029836, Q29678; Q8SNC5; Q951A6; Q9BD38;

10-OCT-2003 (Rel. 42, Lest eaquence update)

10-OCT-2003 (Rel. 42, Last annotation update)

11-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Butheria, Primates; Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                  Y -> D (in allele B*3912).
/rtid=VAR 016659.
S -> A (in allele B*3904 and allele B*3912).
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                                                                                                                                                                                                                                                                        Score 1227; DB 1; Length 362; Pred. No. 1.7e-91;
                                                                                                                                                                                                                                                                                                           32; Indels
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"Molecular diversity of HLA-B.";
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (B*6702).
Iglehart B.A., Leffell M.S.;
"HLA-Bret Decomper-3'UTB).";
Submitted (FEB-2002) to the BMBL/GenBank/DDBJ databases.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOKWAAVVVPSGEEORYTCHVQHEGLPOPLILRW 274
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                                                                                                                                                                                                                                       /FTId=VAR_016421
                                                                                                                                                                                                                                                                    82.0%; Score ....,
81.8%; Pred. No. 1.7e.
tive 18; Mismatches
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                                                                                                                                                                                                                                                                                       Best Local Similarity 81.8
Matches 224; Conservative
 1114
2006
2006
3308
332
1110
1110
283
333
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115
207
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333
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1125
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DISULFID
DISULFID
VARIANT
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                                                      DOMAIN
TRANSMEM
DOMAIN
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N-LINKED (GLCNAC. . .) (BY SIMILARITY).

BY SIMILARITY.

E - G (in allele B*6702).

/FILG-VAR 016536.

I -> V (in allele B*6702).

/FILG-VAR 016538.

/FILG-VAR 016538.

/FILG-VAR 016539.

/FILG-VAR 016539.

/FILG-VAR 01659.

/FILG-VAR 01659.

A -> R (in allele B*6702).

/FILG-VAR 01659.

A -> R (in allele B*6702).

/FILG-VAR 01659.

A -> R (in allele B*6702).

/FILG-VAR 01659.

A -> V (in allele B*6702).

/FILG-VAR 01659.
[4]
SEQUENCE OF 26-206 FROM N.A. (B*6702).
Baldassarre L.A., Hurley C.K.;
Baldassarre L.A., Hurley C.K.;
Novel HLA-B allele (HLA-B*67012 variant).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: Involved in the presentation of foreign antigens to the
                                                                                                                                                        - SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).
- SUBCELLIAR LOCATION: Type I membrane protein.
- POLYNORPHISM: The following alleles of B-67 are known: B*6701 (B-67LAV) and B*6702. The sequence shown is that of B*6701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein; Signal; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3F6A17FC10230F70 CRC64;
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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EMBL; AF321835; AAK09378.1; ---
EMBL; AF321834; AAK09378.1; ---
EMBL; AF50196; AAL18235.1; ---
EMBL; AY050195; AAL18235.1; ---
EMBL; AY050195; AAL18235.1; JOINED.
PIR, 159645; 159645.
HSSP; P30460; 1AGD.
Genew; HGNC:4932; HLA-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM, 142830; ...
InterPro; IRR07110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_c1.
InterPro; IPR001039; MHC_I.
Pfam; PF001047; Ig; I.
Pfam; PF00129; MHC_I:
PRINTS; PR01638; MHCCLASSI.
PRODOM; PD000050; MHC_I; I.
PRODOM; PD000050; MHC_I; I.
PROSITE; PS0035; IG_LIKE; I.
PROSITE; PS00290; IG_MHC; I.
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EMBL; U18789; AAB60360.1; -.
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EMBL; U04787; AAAS3175.1; -.
EMBL; X77658; CAA54739.1; -.
EMBL; L24373; AAA36733.1; -.
EMBL; AJ311601; CAC35319.1; -.
PIR; I37512; S42102.
HSSP; P03989; 1HSA.
                                                                                                                                                                                                                                                                                                                         MIM) 144230;
Interpro; IPR003597; Ig_C1.
Interpro; IPR003597; Ig_C1.
Interpro; IPR003066; Ig_MHC.
Interpro; IPR001039; MHC_I.
Pfam; PF00129; MHC_I.
PRNTS; PR0129; MHC_I.
PRNTS; PR0129; MHCII.
PRNTS; PR0129; MHCII.
PRODOM; PR001050; MHCII.
PRODOM; PR001050; MHCII.
PROSITE; PR001050; MHCII.
PROSITE; PR001050; IG_LIKE; I.
PROSITE; PR001050; IG_LIKE; I.
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363 AA;
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                                                                                        GSHSMRYFYTSVSRPGRGEPRFISVGYVDDTQFVRFDSDAASPREFPRAFWIEQEGFEYW
                                                                                                                                                EWTTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG
                                                            GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
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                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
HLA class I histocompatibility antigen, B-73 alpha chain precursor
(MHC class I antigen B*73).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINES942992929; PubMed=7517915; Vilches C., de Pablo R., Herrero M.J., Moreno M.E., Kreisler M.; Vilches C., de Pablo R., Herrero M.J., Moreno M.E., Kreisler M.; HiA-Bays an atypical HIA-B molecule carrying a Bw6-epitope motif variant and a B pocket identical to HIA-B27.";
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (B*7301).

MEDLINE=95026796; PubMed=7524186;

Parham P., Arnett K.L., Adams B.J., Barber L.D., Domena J.D.,

Stewart D., Hildebrand W.H., Little A.-M.;

"The HLA-B73 antigen has a most unusual structure that defines second lineage of HLA-B alleles.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>.</u>
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-!- FUNCTION: Involved in the presentation of foreign antigens
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  Pred. No. 1.7e-91;
; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          microglobulin).
SUBCELLULAR LOCATION: Type I membrane protein.
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                      18;
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    82.1%;
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                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immune system.
    Similarity
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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ID 1808 HUMAN STANDARD; PRT; 362 AA.

AC P30460; 062901; 095740; 098740; P79542; 095369; 095100; 09GJ20;

AC Q9NY78; 09NYF4; 09T0H6; 09T0M2; 09UQT0;

DT 01-APR-1993 (Rel. 25, Created)
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16; Mismatches 34;
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N-LINKED (GLCNAC. .
BY SIMILARITY.
BY SIMILARITY.
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 Dunckley H.;

Dunckley H.;

Routine HLA-B genotyping with PCR-sequence-specific oligonucleotides

"Routine HLA-B genotyping with PCR-sequence-specific oligonucleotides

(PCR-SSO) detects eight new alleles: B*0807, B*0809, B*1551, B*3529,

B*3532, B*4025, B*5304 and B*5508.";

Tissue Antigens 55:266-270(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                        Shiina S., Tamiya G., Oka A., Inoko H., "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 26-206 FROM N.A. (B*0809; B*0812; B*0813 AND B*0814).
MEDLINE=21276061; PubMed=11380951;
Steiner N.K., Gans C.P., Kosman C., Baldassarre L.A., Edson S.,
Jones P.F., Rizzuto G., Pimtanothai N., Koester R., Mitton W., Ng
Hartzman R.J., Hurley C.K.;
"Novel HIA-B alleles associated with antigens in the 8C CREG.";
01-APR-1993 (Rel. 25, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
HLA class I histocompatibility antigen, B-8 alpha chain precursor (WHC class I antigen B*8).
HLA-B OR HLAB.
                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 26-206 FROW N.A. (B*0807 AND B*0809).
MEDLINE=20236861; PubMed=10777103;
Kennedy C.T., Dodd R., Le T., Wallace R., Ng G., Greville W.D.,
Kennedy A., Taverniti A., Moses J.H., Clow N., Watson N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Elsner H.A., Blasczyk R.; "Identification of the novel allele HLA-B*0809 in a Caucasian individual: estimation of allogeneic potential between B*08
                                                                                                                                                                                                                                                           ಗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bberle M., Lorentzen D., Iwanaga K.K., Watkins D.I.;
"Identification of a new HLA-B*08 variant, B*08NEW.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 26-206 FROM N.A. (B*0806).
Marcos C.Y., Lazaro A.M., Noreen H., Staetny P.;
"New HIA-B locus allele.";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                       SECUENCE FROM N.A. (B*0801).
MEDLINE=89235215; PubMed=2715640;
Parham P., Lawlor D.A., Lomen C.E., Ennis P.D.;
"Diversity and diversification of HLA-A,B,C alleles.";
J. Immunol. 142:3937-3950(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 26-206 FROM N.A. (B*0804).
MEDLINE=97473039; PubMed=931954;
HAPOT R.J. Bratlie A.D. Schreuder G.M., Hurley C.K.;
"Characterization of a novel HLA-B allele, B*0804, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 116-206 FROM N.A. (B*0809).
MEDLINE=20166355; PubMed=10703615;
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SEQUENCE OF 26-206 FROM N.A. (B*0810).
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                                 CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN.
                                                                                         CYTOPLASMIC TAIL.

N-LINED (GLCNAC. . .) (BY SIMILARITY)
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                               81.8%; Score 1224; DB 1; Length 362;
.larity 81.0%; Pred. No. 2.9e-91;
Conservative 21; Mismatches 31; Indels (
                                                                                                                     N -> D (in allele B*0810).

F -> S (in allele B*0810).

F -> S (in allele B*0804).

FTIG=VAR 016503.

S -> N (in allele B*0806).

FTIG=VAR 016504.

FTIG=VAR 016504.

FTIG=VAR 016506.

FTIG=VAR 010506.

S -> T (in allele B*0812).

FTIG=VAR 016506.

S -> T (in allele B*0814).

FTIG=VAR 016507.

N -> YH (in allele B*0814).

FTIG=VAR 016519.

N -> D (in allele B*0814).

FTIG=VAR 016519.

N -> D (in allele B*0817).
                                                                                                                                                                                                                                              / Trid=VAR 016520.

/FTId=VAR 016520.

/ P.D. E (in allele B*0806).

/ FTId=VAR 016509.

D -> L (in allele B*0813).

/FTId=VAR 016510.

/ FTId=VAR 016511.
PROSITE; PS50835; IG_LIXE; 1.
PROSITE; PS00290; IG_MHC; 1.
MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism;
                                                  EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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                                                                          CONNECTING PEPTIDE
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Matches 222; Conserv
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1B42 HUMAN STANDARD; PRT; 362 AA.
301280; P79555;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
110-CCT-2003 (Rel. 42, Last annotation update)
HIA class I histocompatibility antigen, B-42 alpha chain precursor HIA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22512041; PubMed=12622774;
Cox S.T., McWhinnie A.J., Robinson J., Marsh S.G.E., Parham P.,
Madrigal J.A., Little A.M.;
"Cloning and sequencing full-length HLA-B and -C genes.";
Tissue Antigens 61:20-48(2003).
-!- FUNCTION: Involved in the presentation of foreign antigens to
                                                                                                                                                                                                                                                                                           Lardy N.M., Otting N., van de Weerd M.J., van de Horst A.R., Waal L.P., Bontrop R.E., "Full-length CDNA nucleotide sequence of the HLA-B*4202 allele."; Tissue Antigens 50:83-84(1997).
                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                [1]
SEQUENCE FROM N.A. (B*4201),
MEDLINE=89235215; PubMed=2715640;
Parham P., Lawlor D.A., Lomen C.E., Ennis P.D.;
"Diversity and diversification of HLA-A,B,C alleles.";
[2]
265 FQKWAAVVVPSGBEQRYTCHVQHEGLPKPLTLRW 298
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (B*4202).
MEDLINE=97387746; Pubmed=9243763;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (B*4201).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch). immune system.
--- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-subunit):
--- SUBCELLULM LOCATION: Type I membrane protein.
--- SUBCELLULM: The following alleles of B-42 are known: B\*4201 (Bw-42) and B\*4202. The sequence shown is that of B\*4201.

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Pfan, 170011, MHC 1; 1.
PRINTS; PRO1639; MHC 1; 1.
PRODCM; PRO1650; MHC 1; 1.
SMART; SM00407; IGc1; 1.
PROSITE; PSC0835; IG LIKE; 1.
PROSITE; PSC08305; IG MHC; 1.
MHC 1; Transmembrane; Glycoprotein; Signal; Polymorphism. EMBL; M24034; AAA59667.1; -EMBL; M3309194; AAC16437.1; -EMBL; AJ309194; AAC16437.1; -FIR, I61865; I61865.
HSSP; P30460; 1AGD.
GENEW, HGNC.4932; HLA-B.
MIM; 142830; --InterPro; IPR007110; Ig-like. InterPro; IPR003597; Ig\_cl. InterPro; IPR003006; Ig\_MHC. InterPro; IPR001039; MHC\_I. Pfam; PF00047; ig; 1. Pfam; PF00129; MHC I;

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Interpro; IPR007110; Ig-like.
Interpro; IPR003597; Ig_cl.
Interpro; IPR003597; Ig_cl.
Interpro; IPR003006; Ig_MG_I.
Pfam; PP00047; ig; 1.
Pfam; PP00129; MHC_I.
PRINTS; PR01638; MHC_I.
PRODEM; PR00407; IGCLI.
PROSITE; PS06385; IG_LIKE; I.
PROSITE; PS06290; IG_MHC, I.
MHC I; Transmembrane; Glycoprote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40170 MW;
EMBL; X60255; CAA42807.1;
PIR; JH0539; JH0539.
HSSP; P03989; 1HSA.
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1115
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362 AA;
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Best Local S
Matches 224
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MEDLINE=92078860; PubMed=1744581;
Lawlor D.A., Warren E., Taylor P., Parham P.;
Lawlor D.A., Warren E., Taylor P., Parham P.;
"Gorilla class I major histocompatibility complex alleles: comparison to human and chimpanzee class I.";
J. Exp. Med. 174:1491-1509(1991).

J. Exp. Med. 174:1491-1509(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                  GSHSMRYFYISVSRPGRGEPRFISVGYVDDIQFVRFDSDAASPREEPRAPWIEQEGFEYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 EWTTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG
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01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
01-APR-1993 (Rel. 25, Last annotation update)
Class I histocompatibility antigen, GOGO-B0101 alpha chain precursor.
Gorilla gorilla (Lowland gorilla)
Eukaryota; Metazoa; Chordete; Craniate; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                      Gaps
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-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
                      CLASS I HISTOCOMPATIBILITY ANTIGEN
                                                                                                                                                     CYTOPLASMIC TAIL.

N-LINEAD (GLUNAC. . .) (BY SIMILARITY)

N-LINEAD (GLUNAC. . .)

BY SIMILARITY.

BY SIMILARITY.

Y -> H (in allele B*4202).

FTIG=VAR 016460.

C9155AB015DEA1BE CRC64;
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                    HLA CLASS I HISTOCOMPAT:
B-42 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                           Ouery Match
81.8%; Score 1224; DB 1;
Best Local Similarity 81.4%; Pred. No. 2.9e-91;
Matches 223; Conservative 21; Mismatches 30;
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BY SIMILARITY.

N-LINKED (GLCNAC. .) (BY SIMILARITY)

4.19EEE29817165A4 CRC64;
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1847 HUMAN STANDARD; 095392; 09GIL3;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 47, Last annotation update)
11-OCT-2003 (R
                                                  BY SIMILARITY.
CLASS I HISTOCOMPATIBILITY ANTIGEN,
GCGO-BO101 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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81.8%; Pred. No. 3.5e-91;
ive 17; Mismatches 33; Indels C
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MEDLINE=88152906; PubMed=3557938;
Zemmour J., Ennis P.D., Parham P., Dupont B.;
"Comparison of the structure of HLA-BW47 to HLA-B13 and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 265 FQKWAAVVVPSGEEBRYTCHVQHBGLPKPLTLRW 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 FOKWAAVVVPSGEEORYTCHVQHEGLPQPLILRW 274
Glycoprotein; Signal
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SEQUENCE FROM N.A. (A*2301).
MEDLINE-92104637; PubMed=1729171;
Little A.M., Madrigal J.A., Parham P.;
"Molecular definition of an elusive third HLA-A9 molecule: HLA-A9.3.";
Immunogenetics 35:41-45(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205 RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDGTGDTELVETRPAGDRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KDYISLNEDLRSWTAADTVAQITQRFYEABBYABBFRTYLEGGECLELLRRYLENGKETLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 EWITGYAKANAQIDRVALRNILRRYNQSEAGSHTLOGMNGCDMGPDGRLLRGYHQHAYDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECUENCE OF 26-206 FROM N.A. (A*2302 AND A*2303).
MEDLINE=2030230; PubMed=10852390;
BIlis J., Steiner N.K., Kosman C., Henson V., Mitton W., Koester R.,
Ng J., Hartzman R.J., Hurley C.K.;
"Seventeen more novel HLA-A locus alleles.";
"issue Antigens 55:369-373 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                          CYTOPLASMIC TAIL.
N-LINKED (GLCNAC. . .) (BY SIMILARITY).
SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 365 AA.

P30447; QPTQF1; QPTQF8; QPTQG5; QPTQM6;

01-APR-1993 (Rel. 25, Created)

10-APR-1993 (Rel. 25, Last sequence update)

10-OCT-2003 (Rel. 25, Last annotation update)

HIA class I histocompatibility antigen, A-23 alpha chain precursor (FMC class I antigen A*23) (A-9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIA-A OR HLAA.

Homo sapiens (Human).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
                                                                                                                                                                                                                                                          D -> S (in allele B*4702 and allele B*4703).
/FIIGA-VAR 016474.
T -> N (in allele B*4702 and allele B*4703).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1223; DB 1; Length 362; Pred. No. 3.5e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      7FTIG=VAR_016475.

106 107 LR -> RG (In allele B*4702)

7FTIG=VAR_016476.

362 AA; 40571 MW; E3D3E4CBFRG15EAE CRC64;
                 EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 FOKWAAVVVPSGEEORYTCHVQHEGLPQPLILRW 274
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ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.8%;
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                                1114
2206
2298
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1110
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1188
101
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TRANSMEM
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DISULFID
DISULFID
VARIANT
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Best Local
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1A23 HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kosman C.A., Hurley C.K.;
"Novel HIA class I B locus alleles.";
"Novel HIA class I B locus alleles.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Involved in the presentation of foreign antigens to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).
-!- SUBCELIULAR LOCATION: Type I membrane protein.
-!- POLYMORPHISM: The following alleles of B-47 are known: B*4701,
B*4702 and B*4703. The sequence shown is that of B*4701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-302 FROM N.A. (B*4702).

TISSUE-Peripheral blood;

MEDLINE=97316881; PubMed=9174155;

Fischer GF., Broor E., Fae I., Leitner D., Mayr W.R.;

Fischer Sequence analysis of an HLA-B47 variant (HLA-B*4702).";

Tissue Antigens 49:540-542(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20548605; PubNed=11098929; BILLS J.M., Mack S.J., Leke R.F.G., Quakyi I., Johnson A.H., BILIS J.M., Mack S.J., Leke R.F.G., Quakyi I., Johnson A.H., Hurley C.K.; Gemonstrated in class I HLA-A and HLA-B alleles in Cameron, Africa: description of HLA-A*03012, *2612, *3006 and HLA-Tissue Antigens 56:291-302(2000).
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MIM; 142830; -..

MIM; 142830; -..

InterPro; IPR00110; Ig-like.

InterPro; IPR0013006; Ig MHC.

InterPro; IPR001039; MHC_I.

Rean; PP00129; MHC_I.

REAN; PP00129; MHC_I.

REAN; PR00129; MHC_I.

REAN; SNOA97; IG_I.

REAN; SNOA97; IG_I.

REAN; PROSITE; PS00290; IG_MHC; I.

REAN; REAN; IG_MHC; I.

REAN; REA
                                                                                                              TISSUE=Blood;
MEDLINE=22512041; PubMed=12622774;
Cox S.T., McWhinnie A.J., Robinson J., Marsh S.G.E., Parham !
Madrigal J.A., Little A.-M.;
"Cloning and sequencing full-length HLA-B and -C genes.";
Tissue Antigens 61:20-48(2003).
  relationship to 21-hydroxylase deficiency.";
Immunogenetics 27:281-287(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 26-206 FROM N.A. (B*4703).
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EMBL; AJ30898; CAC33087.2; -
EMBL; AJ25141; CAC17463.2; -
EMBL; Y02118; CAA70335.1; -
EMBL; AF016643; AAB70313.1; -
EMBL; AF016643; AAB70313.1; -
EMBL; AF01764; AAB70313.1; -
EMBL; AF071764; AAC23752.1; JOINED.
EMBL; AF071764; AAC23752.1; JOINED.
EMBL; AF071764; AAC23752.1; JOINED.
EMBL; AF071764; AAC23752.1; JOINED.
EMSP; P03989; 1HSA.
                                                                                       SEQUENCE FROM N.A. (B*4701).
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TTW REAR TO BE REAR TO

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1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
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"Novel HLA-B allele.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI TaxID=9606;
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                                                         "Seven novel HLA-A alleles carry previously observed polymorphisms.";
                                                                                                                          microglobulin).
--- SUBCELLULAR LOCATION: Type I membrane protein.
--- POLYMORPHISM: The following alleles of A-23 are known: A*2301,
A*2302, A*2303, A*2304 and A*2305. The sequence shown is that of
                                                                      Tissue Antigens 56:551-552(2000).
-!-FUNCTION: Involved in the presentation of foreign antigens to the immune system.
-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC TAIL.
N-LINKED (GLCNAC. . .) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR003006; Ig-like.

R Interpro; IPR003006; Ig_C1.

R Interpro; IPR003006; Ig_MC.

R Interpro; IPR003006; Ig_MC.

R Interpro; IPR001039; MHC_I.

R Pfam; PF00047; ig; I.

R Pfam; PF00047; ig; I.

R Propom; PD000050; MHC_I; I.

R Propom; PD000050; MHC_I; I.

R Propom; PR000050; MHC_I; I.

R Propom; PR000050; IG-I.

R PROSTIE; PS00290; IG-IKE; I.

R PROSTIE; PS00290; IG_MHC_I: I.

R PROSTIE; PS00290; IG_MHC_I: I.

R PROSTIE; PS00290; IG_MHC; I.

R PROSTIE; PS00290; IG_MHC; I.

R PROSTIE; PS00290; IG_MHC; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
81.8%; Score 1223; DB 1; Length 365;
Best Local Similarity 81.4%; Pred. No. 3.6e-91;
Matches 223; Conservative 19; Mismatches 32; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y--C (in allele A*2305).
/FTIG=VAR 016606.
K--N (in allele A*2303).
/FTIG=VAR 016607.
L--W (in allele A*2302).
/FTIG=VAR 016608.
/FTIG=VAR 016608.
/FTIG=VAR 016608.
/FTIG=VAR 016609.
/FTIG=VAR 016609.
/FTIG=VAR 016609.
/FTIG=VAR 016609.
/FTIG=VAR 016609.
                          Steiner N.K., Edson S.M., Mitton W., Ng J., Hartzman R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A-23 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
     OF 26-206 FROM N.A. (A*2304 AND A*2305)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                  , AF137080, AAD33736.1; --
, AF137079, AAD33736.1; JOINED.
, AF102572; AAD28171.1; --
, AF135549; AAD22272.1; JOINED.
, AF135548; AAD22272.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                AF140860; AAD31878.1; -. AF140859; AAD31878.1; JOINED. 095352; 1HHK.
                  MEDLINE=21068830; PubMed=11169246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40732 MW;
                                                                                                                                                                                                                                                                                                                     EMBL; M64742; AAA03662.1; -.
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                                            Hurley C.K.
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TRANSMEM
DOMAIN
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DISULFID
DISULFID
VARIANT
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EMBL;
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HSSP;
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Gaps

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144
                                                                                                         KDYISLNEDLRSWTAADTVAQITQRFYEAEEYABEFRTYLEGECLELLRRYLENGKETLQ 180
                                           120
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          84
                                                                 181 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT
                                                                                                                                                                                              RIDPPKTHMTHHPISDHEATLRCWALGFYPARITLTWQRDGEDQTQDTELVETRPAGDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (B*3701).
MEDLINE=90207291; PubMed=2320591;
Ennis P.D., Zemmour J., Salter R.D., Parham P.;
Rapid cloning of Hal-A,B CNA by using the polymerase chain
reaction: frequency and nature of errors produced in amplification.";
Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                             EWTTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (B*3704).

TISSUE=Peripheral blood;

MEDLINE=22025782; bubMed=12028544;

BEtefania E., Gomez-Lozano N., de Pablo R., Moreno M.E., Vilches C.;

"Complementary DNA sequence of the novel HLA-B*3704 allele.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immune system.
                                                                                                                                                                                                                                                                                                      PRT; 362 AA.
PIGAGA: 019627; 025HAB; 025HAB; 025HAB; 025HAB; 025HAB; 025HAB; 025HAB; 020131;
01-NOV-1990 (Rel. 16, Leat sequence update)
10-OCT-2003 (Rel. 26, Last sequence update)
HIA class I histocompatibility antigen, B-37 alpha chain precursor (MHC class I antigen B*37).
HIA-B OR HIAB.
HOMO Saplens (Human).
EUKARVATER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       microglobulin).
--- SUBCELLULAR LOCATION: Type I membrane protein.
--- POLYMORPHISM: The following alleles of B-37 are known: B*3701,
B*3704 and B*3705. The sequence shown is that of B*3701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22131949; PubMed=12135437;
Pyo C.-w., Han H., Kim T.G.;
"Identification of a new HLA-B allele, B*3705 containing a Bw6 sequence motif.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-322 FROM N.A. (B*3701).

Hurley C.K., Bei M., Rodriguez S., Johnson A.;

Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                           FOKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRW 298
                                                                                                                                                                                                                                          241 FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 26-206 FROM N.A. (B*3704)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 KDYISLNEDLRSWIAADIVAQIIQRFYEAEEYAEEFRIYLEGECLELLRRYLENGKETLQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 GSHSMRYFHTSVSRPGRGEPRFISVGYVDDTQFVRFDSDAASPRTEPRAPWIEQEGPEYW 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RADPPKAHVAHHPISDHBATLRCWALGFYPAEITLTWQRDGBEQTQDTBLVETRPAGDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTELVETRPAGDRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                       HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC TAIL.
N-LINKED (GLCNAC. . .) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                   81.7%; Score 1222; DB 1; Length 362; 81.4%; Pred. No. 4.3e-91; ive 19; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T -> N (in allele B*3705).
/FIId=VAR 016408.
IR -> RG (in allele B*3705).
/FIId=VAR 016409.
Y -> H (in allele B*3704).
/FIId=VAR_016410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAB4375F05474725 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                     ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
BY SIMILARITY.
T -> N (in all
                                                                                     EMBL, M32320; AAA36233.1; --
EMBL, AF389378; AAL26324.1; --
EMBL, AF418078; AAL26324.1; --
EMBL, AF284828; AAK82990.1; --
EMBL, AF284826; AAK82990.1; --
EMBL, AF284827; AAK82990.1; JOINED.
EMBL, U11267; AAL9221.1; JOINED.
EMBL, AF303102; AAG21400.1; --
EMBL, AF303101; AAG21400.1; --
FIRE, C35997; C35997.
HSSP; P03989; 1HSA.
GGENEW; HGNC:4932; HLA-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      362 AA; 40456 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     107
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DOMAIN
DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
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DISULFID
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Best Local 8
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This SMISS-TROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                        01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
01-APR-1993 (Rel. 25, Last annotation update)
Class I histocompatibility antigen, GOGO-B0102 alpha chain precursor.
Gorilla gorilla gorilla (Lowland gorilla).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Gorilla.
NCBI_TaxID=9595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lawlor D.A., Warren E., Taylor P., Parham P.,
"Gorilla class I major histocompatibility complex alleles: comparison
to human and chimpanzee class I.";
C. Exp. Med. 174:1491-1509(1991).
--- FUNCTION: Involved in the presentation of foreign antigens to the
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188 BY SIMILARITY.
1883 BY SIMILARITY.
110 N-LINKED (GLCMAC. . .) (BY SIMILARITY)
40204 MW, R19EEE2B7CC7BECD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; signal.

4 SI SIMILARITY.
2 CLASS I HISTOCOMPATIBILITY ANTIGEN,
GOGO-BOILOZ ALPHA CHAIN.
4 EXTRACELLULAR ALPHA-1.
5 EXTRACELLULAR ALPHA-1.
3 EXTRACELLULAR ALPHA-1.
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81.8%; Pred. No. 5.1e-91;
ive 16; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONNECTING PEPTIDE
                               265 FQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRW 298
241 FOKWAAVVVPSGEEORYTCHVQHEGLPOPLILRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=92078860; PubMed=1744581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO138; MHCCLASSI.
PRODOM; PRO00050; MHC_1; 1.
SNART; SM0407; IGG1; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
MHC I; Transmembrane; Glycoprote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X60693; CAA41101.1; --
PIR; JH0540; JH0540.
HISSP; P03989; IHSA.
HIGSPP: P03989; IHSA.
HIGSPP: PR007110; Ig_like.
HIGSPP: IPR003300; Ig_C1.
HIGSPP: IPR003006; Ig_MHC.
InterPro; IPR001039; MHC_I.
Pfam; PP00147; Ig; 1.
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Best Local Similarity 81.84
Matches 224; Conservative
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362 AA;
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Oy 61 EWTTGYAKANAQTDRVALENLERRYNOSEAGSHTLOGMNGCDMGPDGRLLRGYHQHAYDG 120

B 5 DRETQTSKAQAQTDRRULRIALRYNQSEAGSHTLOGMNGCDMGPDGRLLRGYHQHAYDG 120

CY 121 KDYISLNEDLSSWTRAADTVAQITQRRYEAEEFRYTEGCHELLRRYLENGKETLO 180

Db 145 KDYIALNEDLSSWTRAADTAAQITQRKWBARRAEQLRAYLEGCTCUELLRRYLENGKETLO 204

CY 181 RADPPRAHVAHHDISDHBATLRCWALGFYPABITLTWQRDGEEQTODTELVETRPAGDGT 240

Db 205 RADTPKTHYTHHPISDHBATLRCWALGFYPABITLTWQRDGEDQTQDTELVETRPAGDGT 264

CY 241 FOKWAAVVVPSGEEGRYTCHVQHEGLPQPLILRW 274

Db 265 FQKWAAVVVPSGEERRYTCHVQHEGLPQPLILRW 298

Search completed: June 18, 2004, 19:25:59
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Title: Perfect score:

Run on:

Scoring table: Sequence:

Searched:

Database

Result

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019589 homo sapien 0993/1 homo sapien 0993/1 homo sapien 0993/1 homo sapien 0993/1 homo sapien 070/20 homo sapien 080/20 homo sapien 080/20 homo sapien 080/20 homo sapien 090/20 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 7; Length 324;
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THE X., Xu L., Liu Y., Zeng Y.;

THE X., Xu L., Liu Y., Zeng Y.;

THE X., Xu L., Liu Y., Zeng Y.;

Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

BEMBL; AV216682; D. C. membrane; IEA.

GO; GO:0016020; C. membrane; IEA.

GO; GO:0016025; D. immune response; IEA.

RILETPRO; IPR00104; Crystallin.

InterPro; IPR00104; Crystallin.

InterPro; IPR001039; MHC.

I
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Nonclassical MHC class I antigen (Fragment).
HLA-F.
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                       019589
099MXD1
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095471
0974786
08M4G3
099553
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099774
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095412
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Query Match
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Q861F0;
   SOUR BEAUTH OF THE PROPERTY OF
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Q861£9 homo sapien
Q88Mp5 homo sapien
Q95hc0 homo sapien
Q95ft2 homo sapien
Q95ft2 pan troglod
Q97x27 pan troglod
Q19692 homo sapien
Q7812 homo sapien
Q78189 homo sapien
Q29705 homo sapien
Q29705 homo sapien
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homo sapien
homo sapien
homo sapien
pan troglod
homo sapien
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Q29934
Q9mxi2
                                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1017041 segs, 315518202 residues
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1: Sp_acteria:*

3: sp_bacteria:*

4: sp_human:*

5: sp_invertebrate:*

5: sp_mammal:*

5: sp_mammal:*

5: sp_maganelle:*

5: sp_phage:*

5: sp_phage:*

5: sp_plant:*

5: sp_plant:*

5: sp_rodent:*

5: sp_vrius:*

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Q8MLP5
Q95HC0
Q8MG21
Q95HC2
Q95HC2
Q95HC3
Q95HC3
Q95HC3
Q95HC3
Q19692
Q19692
Q19692
Q29705
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Q29934
Q9MXI2
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
Listing first 45 su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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1496
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KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRIYLEGECLELLRRYLENGKETLQ 180
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
He X., Xu L., Liu Y., Zeng Y.;
"Cloning of full-length HLA-F*0101 variant 2 cDNA from Han Chinese.";
Submitted (MARA-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AF523285; AAM/4980.1; --
EMBL; AF523286; AAM/4981.1; --
EMBL; AF523287; AAM/4981.1; --
EMBL; AF523287; AAM/4982.1; --
                                                                                                                                                                                  SEQUENCE FROM N.A.
Ishitani A., Miki A., Williams L.M., Moore Y., Geraghty D.E.;
"Hiha-E, F, and G polymorphism: genomic sequence defines new variation spanning the nonclassical class I genes.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         He X., Liu Y., Xu L., Zeng Y., "Cloning of full-length HLA-F*0101 variant 1 cDNA from Han Chinese."; Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Last annotation update)
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Pred. No. 2.9e-122;
                                                                                                                                                                                                                                                                  241 FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
                                                                                                                                                                                                                                                                                                        258 FQKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 291
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EMBL: AXESSEDS; AMOSSO74.1; -.

GO, GO:0016020; C:membrane; IEA.

GO, GO:0016020; C:membrane; IEA.

GO, GO:0016020; F:membrane; IEA.

INTERPRO: IPRO0110; Ig-like.

INTERPRO: IPRO0110; Ig-like.

INTERPRO: IPRO0139; MHC.

INTERPRO: IPRO0139; MHC.

INTERPRO: IPRO0139; MHC.

PEAM; PRO0129; MHC.

PROMITS; PRO1639; MHC.

PROSITE; PS00225; CRYSTALIN BETAGANMA; 1.

PROSITE; PS00229; IG-LKE; 1.

PROSITE; PS00229; IG-MHC.; 1.
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01-MAR-2002 (TrEMBLrel. 20, La
01-OCT-2003 (TrEMBLrel. 25, Lan
MHC class Ib antigen.
HLA-F.
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AAM74985.1;
AAM74988.1;
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AAM74990.1;
AAM74991.1;
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Best Local Similarity
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AF523295;
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Q8WLP5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLIWQRDGESQTQDTELVETRPAGDGT 257
                                                                                                                                                                                                                  EWTTGYAKANAQTDRVALRNILRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 120
                                                                                                                                                                                                                                                            EWITGYAKANAQIDRVALRNILRRYNQSEAGSHILQGMNGCDMGPDGRLLRGYHQHAYDG 137
                                                                                                                                                                                                                                                                                                                             KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQ 180
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                                                                                                                                                       18 GSHSLRYFSTAVSRÞGRGEPRYIAVEXVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 77
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu Y., Xu L., Zeng Y., He X.;
Liu Y., Xu L., Zeng Y., He X.;
In A new polymorphism in non-classical MHC class I HLA-F.";
Submitteed (JAM-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY221102; AA034407.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
InterPro; IPR001010; Ig-like.
R InterPro; IPR003597; Ig-cl.
R InterPro; IPR003006; Ig MHC.
R InterPro; IPR003006; Ig MHC.
                       2.6e-122;
nes 0; Indels
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324 AA; 36518 MW; E3E028177D2716F4 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
MHC class I antigen (Fragment).
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Pfam; PF00129; MHC 1; 1.
PRINTS, PR01638; MHCCLASI.
PRODOM; PD000050; MHCCL, 1.
SMART; SM00407; IGG1; 1.
PROSITE; PS00225; CRYSTALLIN BETAGAMWA; 1.
PROSITE; PS00235; IGLIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
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                    Pred. No. 2.6; Mismatches
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100.08; Pr.
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142 KDYISLNEDLRSWTAADTVAQITQRFYEAEFYAEEFRTYLEGECLELLRRYLENGKETLQ
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Last annotation update)
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Pred, No. 7.9e-122;
0; Mismatches 1;
                                                                           241 FOXWAAVVVPSGEEORYTCHVQHEGLPOPLILRW 274
                                                                                                  FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 295
                                                                                                                                                                  346 AA.
                                                                                                                                                                                           Created)
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Les 273; Conservative
                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                       01-0CT-2002 (TrEMBLrel.
01-0CT-2002 (TrEMBLrel.
01-0CT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                MHC class Ib antigen.
HLA-F.
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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Matches
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                                                                                                  EWITGYAKANAQIDRVALRNILRRYNQSBAGSHTLQGMNGCDMGPDGRILRGYHQHAYDG 141
                                                                                                                               KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQ 180
                                                                                                                                                                                                        202 RADPPKAHVAHHPISDHEATLRCWALGFYPABITLTWQRDGBEQTQDTELVETRPAGDGT 261
                                                                             EWITGYAKANAQIDRVALRNLLRRYNQSEAGSHILQGMNGCDMGPDGRLLRGYHQHAYDG 120
                                                                                                                                                      142 KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQ 201
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                                                    GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 81
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                             GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTOFLRFDSDAAIPRMEPREPWVEOEGPOYW
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    Gaps
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01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to major histocompatibility complex, class I, F.
Buhon sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Straubberg R.;
Submitted (JUV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC009260; AAH09260.1; -.
GC); GO:00166021; C:integral to membrane; IEA.
GC); GO:0016021; P:immune response; IEA.
InterPro; IPR0011064; Crystallin.
InterPro; IPR0011064; Crystallin.
InterPro; IPR001064; Grystallin.
InterPro; IPR001069; Ig-dl.
InterPro; IPR001089; Ig-dl.
InterPro; IPR001089; MHC.
InterPro; IPR001099; MHC.
InterPro; IPR001099; MHC.
InterPro; IPR001099; MHC.I:
Pfam; PF00129; MHC I: 1.
Pfam; PF00109; MHC I: 1.
Pram; PF00109; MHC I: 1.
PRMTMS; PR01089; MHCI: 1.
PR01IE; PS00129; GC RYSTALIN BETAGAWMA; I.
PROSITE; PS00255; GC KRYSTALIN BETAGAWMA; I.
PROSITE; PS00295; IG LME; I.
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    0; Indels
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100.0%; Pred. No. 4.1e-122;
ive 0; Mismatches 0;
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    Mismatches
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    274; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 KDYISINEDIRSWTAADTVAQITORFYEABEYAEEFRTYLEGECLELLRRYLENGKETLQ 180
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               RADP PKAHVAHHP I SDHEATLRCWALGFYPAE I TL TWQRDGEEQTQDTELVETRPAGDGT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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O7YR27;
01-OCT-2003 (
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01-OCT-2003 (
Class Ib.
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01-DEC-2001 (
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01-OCT-2003 (
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

LOUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE INMUNE SYSTEM (BY SIMILARITY).

MICHOGOGOGOSTI SIMILARITY).

EMBL; AL022723; CAB46623.1; -

MICHOGOGOSTI, G.: Antegral to membrane; IEA.

GO; GO:0016021; G.: Antegral to membrane; IEA.

GO; GO:0016021; G.: Antegral to membrane; IEA.

GO; GO:0016021; G.: Antegral to membrane; IEA.

INTERPRO; IPRO0110; IG-11ke.

INTERPRO; IPRO0104; CYSTALIA.

INTERPRO; IPRO0129; MHC_I.

INTERPRO; IPRO0129; MHC_I.

INTERPRO; IPRO0129; MHC_I.

INTERPRO; PRO1029; MHC_I.

SWART; SMO0407; IGGL; I.

SWART; SMO0407; IGGL; I.

SWART; SMO0407; IGGL; I.

BROSITE; PSO0225; CRYSTALIN BETAGAWMA; I.

ROSITE; PSO0225; GRYSTALIN BETAGAWMA; I.
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261
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RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 25, Last annotation update)
DJ377H14.9 (Major histocompatibility complex, class I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362 AA; 40578 MW; 970D072C813A07E2 CRC64;
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                                                 FOKWAAVVVPSGEEORYTCHVQHEGLPOPLILRW 274
                                                                              262 FOKWAAVVVPPGEEORYTCHVOHEGLPOPLILRW
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Matches 273; Conservative
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SEQUENCE 362 AA; 40578 M
                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 EWTTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG
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                                                                                                                                                                                                 Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                            major histocompatibility
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                                                                                                                                                                         Pan troglodytes (Chimpanzee).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0ECF12B7DB17B814 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.7%; Score 1477; DB 7;
99.3%; Pred. No. 1.3e-120;
ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
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                                                                                                                                                                                                                                                                                                               MEDLINE=21291697; PubMed=11398964; Adams E.1., Parham P.; Adams E.J., Parham P.; Adams E.J., Parham P.; Genmon chimpanzee major hi "Genomic analysis of common chimpanzee major hi complex class I genes."; Immunogenetics 53:200-208(2001).

EMBL; AF338355; AAK7479-11; GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016025; P:immune response; IEA.

InterPro; IPR00110; Ig-like.

InterPro; IPR00110; Ig-like.

InterPro; IPR001309; Ig-Like.

InterPro; IPR001309; Ig-Like.

InterPro; IPR001309; MHC_I.

Pfam; PF00129; MHC_I.

Pfam; PF00129; MHC_I.
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ProDom; PD000050; MHC_1; 1.
SMART; SM00407; IGGL; 1.
PROSITE; PS00225; CYSTALLIN BETAGAMMA; 1.
PROSITE; PS00295; IG LIKE; 1.
PROSITE; PS00290; IG MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 362
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(TrEMBLrel. 25, Last seqn
(TrEMBLrel. 25, Last anno
PRT;
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                                             (TrEMBLrel. 19, (TrEMBLrel. 19, (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.3
Matches 272; Conservative
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PRELIMINARY;
                                                                                                                      MHC class I antigen.
PATR-F.
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us-09-819-371-5.rspt

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Hasegawa T., Sugahara Y., Moriyama Y., Nanzai H., Ogawa A., Tawara K.,
Kondo S., Tokunaga K.;
Kondo S., Tokunaga K.;
Molecular characterization of a novel HLA-B27 allele.";
Molecular characterization of a novel HLA-B27 allele.";
Submitted (JaN-1996) to the EMBL/GenBank/DDBJ databases.
Incharacterization of a novel HLA-B27 allele.";
Submitted (JaN-1996) to the EMBL/GenBank/DDBJ databases.
Incharacterization of a novel HLA-B27 allele.";
SIMMINS SYSTEM (BY SIMILARITY).
INCOGLOBULIN (BY SIMILARITY).

REMEL; DB3043; BAA11753.1; -.
REMEL; DB3043; BAA11753.1; -.
REMEL; DB3043; BAA11753.1; -.
REMEL; DB30631; C:integral to membrane; IEA.
RO; GO:0016021; C:integral to membrane; IEA.
RO; GO:0016021; C:integral to membrane; IEA.
RO; GO:0016051; PR:immune response; IEA.
RICHERPO; IPR003006; Ig-HRC.
RICHERPO; IPR003006; Ig-HRC.
RICHERPO; IPR003006; Ig-MRC.
RICHERPO; IPR003006; Ig-MRC.
RICHERPO; IPR003006; Ig-MRC.
RICHERPO; IPR003006; IG-MRC.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0C9A7A4902383219 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.9%; Score 1240; DB 7;
82.8%; Pred. No. 4.6e-100;
iive 14; Mismatches 33;
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC_I.
Pfan; PF00047; ig; 1.
Pfan; PF00129; MHC_I; 1.
PRINTS; PR01638; MHCCLASSI.
ProDom; PR0060050; MHC I; 1.
PROSITE; PS00803; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
Glycoprotein; Transmembrane.
NON TER 274 274
SEQUENCE 274 AA; 31659 NW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31659 MW;
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03,
25,
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Best Local Similarity 82.88
Marches 227; Conservative
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01-MAY-1997 (TrEMBLrel.
01-MAY-1997 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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HLA-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Blood;
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MEDLINES # **PODAGE **PODAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTÖFLRFDSDAAIPRMEPREPWVEQEGPQYW
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                                                                                                                                                                                                                                                                         MEDLINE=22709114; PubMed=12799463; MEDLINE=22709114; PubMed=12799463; MEDLINE=22709114; PubMed=12799463; Anzal T., Shina T., Kimura N., Yanagaya K., Kohara S., Shigenari A., Yamagara T., Kulki J.K., Naruse T.K., Fujimori Y., Fukuzumi Y., Yamazaki M., Tashiro H., Iwamoto C., Umehara Y., Imanishi T., Meyer A., Ikeo K., Goljobori T., Bahrama S., Inoko H., Goljobori T., Bahrama S., Inoko H., "Comparative sequencing of human and chimpanzee MHC class I regions unveils insertions/deletions as the major path to genomic
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                            Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           divergence.";
Proc. Natl. Acad. Sci. U.S.A. 100:7708-7713(2003).
EMBL: AB100087; BAC78191.1; -
SEQUENCE 362 AA; 40625 MW; BAS699D08181A1FF CRC64;
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362 AA; 40486 MW; BC00FC372955711D CRC64;
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Q29705;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                              Length 362;
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                                                                                                                                                    362 AA; 40441 MW; 3CA65547E65FDF84 CRC64;
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Last annotation update)
                                                                                                                                                                                          82.9%; Score 1240; DB 7;
82.5%; Pred. No. 6.8e-100;
live 18; Mismatches 30;
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InterPro; IPR003109; Ig-1ike.
InterPro; IPR001039; MHC. InterPro; IPR001039; MHC. I. Pfam; PF001047; Ig. 1.
Pfam; PF00129; MHC. I. 1.
PRINTS; PR01628; MHC. I. 1.
PROSTIF; PR01638; MHC. I. 1.
PROSTIF; PS00290; IG. MHC; I. 1.
Glycoprotein; Transmembrane.
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                                                                                PROSITE; PSC0835; IG LIKE; I. PROSITE; PSC0290; IG MHC; I. Glycoprotein; Transmembrane. SEQUENCE 362 AA; 40441 MM;
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    Pfam; PF00129; MHC I; 1.
PRINTS; PR01638; MHCCLASSI.
ProDom; PD000050; MHC_I; 1.
SMART; SM00407; IGc1; 1.
                                                                                                                                                                                                                Local Similarity 82.5
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                                                                                                                            25 GSHSWRYFHISVSRPGRGEPREITVGYVDDTLFVRFDSDAASPREEPRAFWIEQEGPEYW 84
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1015_TaxID=9606;
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82.5%; Pred. No. 8.3e-100;
ive 16; Mismatches 32; Indels (
       Length 362;
82.9%; Score 1240; DB 7; Length 3
82.8%; Pred. No. 6.8e-100;
ive 14; Mismatches 33; Indels
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MHC CLASS I ANTIGEN HLA-B.
148B56561595A505 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
MHC class I antigen HLA-B precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 FOKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 274
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GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016025; P:immune response; IEA.

InterPro; IPR07110; Ig-11.

InterPro; IPR03597; Ig_C1.

InterPro; IPR003006; Ig MHC.

InterPro; IPR01039; MHC_I.

Pfam; PF00129; MHC_I.
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25 362 M
362 AA; 40479 MW;
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PRINTS; PR01638; MHCCLASSI.
ProDom; PD000050; MHC_I; 1.
PROSTIE; PS00290; IG_NHC; 1.
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Matches 226; Conservative
                          Best Local Similarity 82.8 Matches 227; Conservative
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WEDLINE=2032475; PubMed=10866106; Matkins D.I., Doxiadis G.G.M., Angulene and a Grot N.G., Otting N.P., Arguello R., Watkins D.I., Doxiadis G.G.M., Andrigal J.A., Bontrop R.E.; Madrigal J.A., Bontrop R.E.; Madrigal J.A., Bontrop R.E.; Major histocompatibility complex class I diversity in a West African R.T. chimpanzee population: implications for HIV research."; R. Immunogenetics 51:398-4090[2000].

Immunogenetics 51:398-4090[2000].

Immunogenetics 51:398-4090[2000].

Immunogenetics 51:398-4090[2000].

Inmunogenetics 51:398-4090[2000].

Immunogenetics 51:398-4090[2000].
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                                                                   77 EEQTRNAKANAQTDRVSLGNLRRYYNQSEGGSHTVQIMYGCDLGFDGRLLRGYHQFAYDG
                                                                                                                                                                                                                                                             137 KDYIALNEDLRSWTAADMAAQNTQRKWEGDRYAERPRAYLEGRCVEWLRRYLENGKETLQ
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                             EWTTGYAKANAQTDRVALRNILRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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; Pred. No. 1.2e-99;
15; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 FOXWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          257 FOKWGAVVVPSGEEORYTCHVOHEGLPEPLTLRW 290
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PERMY, PRO0129; WHC I; I.

PERMY, PRO1839; MHCCLASSI.

PEDDOM; PD000050; MHC I; I.

CMART: SM00407; IGC1; I.
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SEQUENCE 362 AA; 40442 MW;
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PROSITE; PS00290; IG MHC; 1.
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82.8%;
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01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2003 (TrEMBLrel. 25,
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EWITGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 120
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12)

13. VITOL. 70:7339-7340(1990).

14. VISOL. 70:7339-7340(1990).

15. VISOL. 70:7339-7340(1990).

15. VORS G., LECVIN N.A.,

15. VORS G., LECVIN N.A.,

16. SUDMITCHE GRAR-2000) to the EMBL/GenBank/DDBJ databases.

16. SUDMITCHE SYSTEM RESENTATION OF FOREIGN ANTIGENS TO THE TRANSPORT OF THE OF T
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01-0CT-2003 (TTENBLrel. 25, Last annotation update)
MHC class I antigen Manu-B*12 (Fragment).
Macaca mulatta (Rhesus macaque).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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SEQUENCE FROM N.A.
MEDLINE-96386644; PubMed=8794394;
VOSS G., Letvin N.L.;
"Definition of human immunodeficiency virus type 1 gp120 and cytotoxic T-lymphocyte epitopes and their restricting major cytotoxic T-lymphocyte epitopes and their restricting major histocompatibility complex class I alleles in simian-human immunodeficiency virus-infected rhesus monkeys.";
J. Virol. 70:7335-7340(1996).
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82.1%; Pred. No. 1.2e-99;
iive 15; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FOXMAAVVVPSGEEQRYTCHVQHEGLPKPLTLRW 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 15, Created) (TrEMBLrel. 15, Last seq (TrEMBLrel. 25, Last ann
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ses 225; Conservative
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Tallelic series...;

Droc. Natl. Acad. Sci. U.S.A. 83:1428-1432 (1986).

1. FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE INVOLVED IN THE PRESENTATION OF SIMILARITY).

BMBL; MIZEOGLOBULIN (BY SIMILARITY).

BMBL; MIZEOGLOBULIN (BY SIMILARITY).

BMBL; MIZEOGLOBULIN (BY SIMILARITY).

BMBL; MIZEOROSSS; P:immune response; IEA.

GO; GO:0016621; C:integral to membrane; IEA.

GO; GO:0016621; C:integral to membrane; IEA.

GO; GO:0016621; C:integral to membrane; IEA.

R InterPro: IPR001359; Pilke...

INTERPRO: IPR001359; MHC_I.

R PFEM: PFC00129; MHC_I:

R PFEM: PFEM
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                                           RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLIWQRDGEEQTQDTELVETRPAGDGT 240
                                                                                                                                                                                                           205 RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGBDQTQDTELVETRFAGDRT 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
MEDLINE=86149317; PubMed=3485286;
Szots H., Riethmuller G., Weiss E., Meo T.;
Complete sequence of HLA-B27 cDNA identified through the characterization of structural markers unique to the HLA-A, -B, and -C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Matches 226; Conservative 14; Mismatches 34; Indels
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PROSITE; PS00290; IG_MHC; 1.
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SEQUENCE 359 AA, 40042 M
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Qy 181 RADPPKAHVAHHPISDHEATLRCWALGFYPABITLTWQRDGEBGTQDTELVETRPAGDGT 240

Db 202 RVDPPKTHVTHPISDHEATLRCWALGFYPABITLTWQRDGEBQTQDTELVBTRPAGDGT 261

Qy 241 FQKWAAVVVBGGEBQRYTCHVQHEGLPQPLILRW 274

Db 262 FQKWAAVVVPSGEBQRYTCHVQHEGLPKPLTLRW 295

Search completed: June 18, 2004, 19:28:05

Job time: 47 secs
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Sequence 187, Appl
Sequence 1431, Ap
Sequence 4, Appli
Sequence 4, Appli
Sequence 4063, Ap
Sequence 30718, A
Sequence 31089, A
Sequence 31089, A
Sequence 335, App
Sequence 35, App
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1 GSHSLRYFSTAVSRPGRGEP......QRYTCHVQHEGLPQPLILRW 274
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_RW PUBL.pep:*

3: /cgn2_6/ptodata/2/pubpaa/SPCT_RW PUBL.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

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GenCore version 5.1.6
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Sequence 38005, A Sequence 5, Appli Sequence 8, Appli Sequence 3648, Ap	8 8 8 6 7 8 9 8 9 8 9 8 9 8 9 8 9 8 9 8 9 8 9 8	Sequence 22, Appl
9 US-09-864-761-38005 12 US-10-380-880-5 12 US-10-380-880-8 15 US-10-380-880-8 15 US-10-104-047-3648 12 US-10-380-880-7		14 US-10-138-888-22
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## ALIGNMENTS

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US-09-819-371-5
Sequence 5, Application US/09819371
Publication No. US20040053344A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Cartille OF INVENTION: Using Thereof
TITLE OF INVENTION: Using Thereof
TITLE OF INVENTION: US/09/819,371
CURRENT APPLICATION NUMBER: US/09/819,371
CURRENT FILING DATE: 2002-03-15
NUMBER OF SEQ ID NOS: 6
SOUTWARE: Patentin version 3.0
SEQ ID NO 5
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                                                                                                                                                                                                                                                                                                                                                            LENGTH: 274
TYPE: PRT
CRGANISM: Homo sapiens
US-09-819-371-5
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US-10-029-186-31089
US-10-029-186-31089
US-10-029-186-31089
Sequence 31089, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: HANDEN GENERSSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-K-Z
CURRENT APPLICATION UNDER: US/10/029,386
CURRENT APPLICATION UNDER: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
LENGTH: 91
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Sequence 835, Application US/09925302

Sequence 835, Application US/09925302

GENERAL INFORMATION:

TITLE DE INFORMATION:

TITLE DE INFORMATION:

CURRENT APPLICATION NUMBER: US/09/925,302

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: OFT/US00/05918

PRIOR PILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

NUMBER: OF SEQ ID NOS: 896

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 835

INFERIOR INFORMATION NUMBER: DEBOTH OF SEQ ID NOS: 896

SEQ ID NO 835

TYPE: PRT
                                                                                                                                                                                                                           Length 77;
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                                                                                                                                                                                                                                                                                                                                         224 QIQDIELVETRPAGDGTFQKWAAVVVPSGEEQRYICHVQHEGLP 267
                             FEATURE:
CHER INFORMATION: MAP TO CHR6.1
CHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 53
CHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9.4
COTHER INFORMATION: SWISSPROT HIT: P30507, EVALUE 6.00e-42
US-10-029-386-34273
                                                                                                                                                                                                                           Query Match
16.1%; Score 44; DB 14; Length 77
Best Local Similarity 100.0%; Pred. No. 7.3e-36;
Matches 44; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT

GRGANIGM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC004204.1
GOTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
OTHER INFORMATION: SWISSPROT HIT: P30509, EVALUE 1.000-55 US-10-029-386-3108
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100.0%; Pred. No. 8.5e-36;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                      25 QTQDTELVBTRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 QTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 44; Conservative
     ORGANISM: Homo sapiens
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Sequence 30718, Application US/10029386

Publication No. US20030194704A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION UNMER: US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3473, Application US/1029386
| Publication No. US20030194704A1
| GENERAL INPORMATION:
| APPLICANT: Fenn, Sharron G. | APPLICANT: Penn, Sharron G. | APPLICANT: Pannk, David R. |
| APPLICANT: Pannk, David R. | APPLICANT: Pannel, David R. |
| TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR (FILE REFERENCE: AEOMICA-X-2 | TITLE OF INVENTION: WINDERS US/10/029,386 | CURRENT APPLICATION NUMBER: US/10/029,386 | CURRENT FILING DATE: 201-12-20 | NUMBER OF SEQ ID NOS: 34288 | SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids US-10-264-049-4063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                              66 YAKANAQIDRVALRNILRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDGKDYIS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 DPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGTFQ 242
                                                                                                                                                                                                                                                   1 YAKANAQIDRVALRNILRRYNQSEAGSHILQGMNGCDMGPDGRLLRGYHQHAYDGKDYIS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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                                                                                                                                              Gaps
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                                                                                                                                              ö
                                                                                Query Match 25.5%; Score 70; DB 15; Length 186; Best Local Similarity 100.0%; Pred. No. 1.7e-61; Matches 70; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 24.8%; Score 68; DB 14; Length 96; Best Local Similarity 100.0%; Pred. No. 9.4e-60; Matches 68; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: MAP TO CHR6.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12
OTHER INFORMATION: SWISSPROT HIT: P30511, EVALUE 2.00e-52
                                                                                                                                                                                                                                                                                                            126 LNEDLRSWIA 135
                                                                                                                                                                                                                                                                                                                                                                 61 LNEDLRSWTA 70
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 KWAAVVVP 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KWAAVVVP 69
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LENGTH: 77
TYPE: PRT
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LENGTH: 96
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APPLICANT: ALIERMAN, ARIEN
APPLICANT: MAISANKAI, UTGE1
APPLICANT: MAISANKAI, UTGE1
APPLICANT: MACDOUGAII, JOHN
APPLICANT: MACDOUGAII, JOHN
APPLICANT: ALSODE, DAVIG
APPLICANT: ALSODE, DAVIG
APPLICANT: LEDISY, DENISE et al.
TITIES OF INVESTION: THERAPEUTIC FOLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHO
FILER REFERENCE: 21402-446 A.
CURRENT APPLICATION NUMBER: 06/309,501
PRIOR PELLORICATION NUMBER: 60/309,501
PRIOR PELLORICATION NUMBER: 60/303,994
PRIOR PELLORICATION NUMBER: 60/313,994
PRIOR APPLICATION NUMBER: 60/313,914
PRIOR APPLICATION NUMBER: 60/310,291
PRIOR PELLNG DATE: 2001-08-03
PRIOR FILING DATE: 2001-08-07
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-07
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14.6%; Score 40; DB 14; Length 78;
Best Local Similarity 100.0%; Pred. No. 7.3e-32;
Matches 40; Conservative 0; Mismatches 0; Indels
EXPRESSED IN PLACENTA, SIGNAL = 48
EXPRESSED IN FETAL LIVER, SIGNAL = 11
EXPRESSED IN LUGS, SIGNAL = 57
WISSPROT HIT: P30507, EVALUE 7.00e-24
                                                                                                                                                                                                                                                                                                                                                                      228 TELVETRPAGDGTFOXWAAVVVPSGEEORYTCHVOHEGLP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                            29 TELVETRPÁGDGTFOKWAAVVVPSGEEQRYTCHVQHEGLP 68
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PRIOR FILING DATE: 2001-08-17
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PRIOR APPLICATION NUMBER: 60/312,892
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Ji, Weizhen
Padigaru, Muralidhara
Casman, Stacie
Voss, Edward
Boldog, Perenc
Gorman, Linda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rieger, Daniel
Shimkets, Richard
Zerhusen, Bryan
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Rastelli, Luca
Spytek, Kimberly
Edinger, Shlomit
Ellerman, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kekuda, Ramesh
APPLICANT: Miller, Charles
APPLICANT: Patturajan, Meera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leite, Mario
Vernet, Corine
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Gerlach, Vale
Tord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pena, Carol
       OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: S
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GENERAL INFORMATION:
                                                                                                                                                           US-10-029-386-30752
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US-10-210-172-156
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Sequence 30752, Application US/10029386
| Sequence 30752, Application US/10029386
| Publication No. US20030194704A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Penn, Sharron G. |
| APPLICANT: Pank, David R. |
| APPLICANT: Penn, Sharron G. |
| APPLICANT: Penn, Savience. AND GENOME-PENN GENOME COURTENT FILING DATE: 2001-12-20 |
| NUMBER OF SEQ ID NOS: 34288 |
| SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 |
| LENTER FILING DATE: COURTEND GENOME COURTEND GENOME
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JTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                              FEATURE:

NAME/KEY: SITE

LOCATION: (95)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-835
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Sequence 835, Application US/09925302

Publication No. US20030064072A9

GENERAL INFORMATION:

APPLICANT: ROSEN et al.

ITILE OF INVENTION:

TILE REFERENCE: PA104

CURRENT APPLICATION NUMBER: US/09/925,302

CURRENT APPLICATION NUMBER: PCT/US00/05918

PRIOR FLING DATE: 2001-08-10

PRIOR FLING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 896

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 835

LENGTH: 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             224 QTQDTELVETRPAGDGTFQXWAAVVVPSGBEQRYTCHVQHEGLP 267
                                                                                                                                                                                                                                                                                Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                            224 QTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 267
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                                                                                                                                                                                                                                                                            Query Match
16.1%; Score 44; DB 9; Length 104
Best Local Similarity 100.0%; Pred. No. 9.6e-36;
Matches 44; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 QTQDTELVETRPAGDGTFQKWAAVVVPSGBEGRYTCHVQHEGLP 75
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OTHER INFORMATION: MAP TO CHR6.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 8.7
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 44; Conserv
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LOCATION: (95)
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US-09-925-302-835
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Sequence 72, Application US/10085198
Publication No. US20040009907A1

GENERAL INFORMATION:

TITLE OF INVENTION:

FILE REFERENCE:

CURRENT FILING DATE:

CURRENT PELLING DATE:

PRIOR PELLOR NUMBER:

60/211,646

PRIOR PELLING DATE:

2001-03-16

PRIOR PELLING DATE:

2001-08-13

PRIOR PELLING DATE:

2001-08-16

PRIOR PELLING DATE:

2001-03-26

PRIOR PELLING DATE:

2001-03-16

PRIOR PELLING DATE:

2001-03-16

PRIOR PELLING DATE:

2001-08-16

PRIOR PELLING DATE:

2001-03-20

PRIOR PELLING DATE:

2001-04-21

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2001-06-20

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2001-06-20

PRIOR PELLING DATE:

2001-06-20

PRIOR PELLING DATE:

2001-06-20

PRIOR APPLICATION NUMBER:

60/215,614

PRIOR PELLING DATE:

2001-06-20

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2001-06-20

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2001-08-20

PRIOR
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PRIOR FILING DATE: 2001-08-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 327
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 156
LENGTH: 371
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14.6%; Score 40; DB 15; Length 371;
Best Local Similarity 100.0%; Pred. No. 3e-31;
Matches 40; Conservative 0; Mismatches 0; Indels
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; ORGANISM: Homo sapiens
US-10-085-198-72
                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
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This invention relates to a cancer cell specific HLA-F antigen. The invention includes DNA encoding the antigen, and a method for the preparation of the cancer cell specific HLA-F antigen. The antigen may be used in a method to diagnose cancer, in which the protein is used to detect anti-HLA-F antibodies in bodily fluids of the patient. The present sequence represents the cancer cell-specific HLA-F antigen of the
                                      Human pro
HLA-G rec
Human Pro
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Abg37468 Human p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.
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AAMO 5976
ABG40192
AAU79455
AAU79455
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ADB65494
ADB65494
ADB70551
ABB70687
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                                                                                                                                                                                                                                                                        AAG64618 standard; protein; 274 AA
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  WPI; 2001-360493/38.
N-PSDB; AAH45556.
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MEDINET KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KIMURA K.
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Best Local Simil
Matches 274;
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  invention
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Abp42931 Human ova
Aab84297 Lung canc
Aab8491 Consensus
Aar12466 Hinan ova
Aay7033 Breast can
Aay7033 Breast can
Aay13283 Novel hum
Aab9793 Human she
Ad631177 Human dia
Ad64250 Human NoV
Aam18379 Peptide #
Abb37410 Peptide #
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                                                                      June 18, 2004, 19:26:06; Search time 61 Seconds (without alignments) 1269.148 Million cell updates/sec
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1 GSHSLRYFSTAVSRPGRGEP.....QRYTCHVQHEGLPQPLILRW
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Compugen Ltd.
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            GenCore version
Copyright (c) 1993 - 2004
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Result

261

274

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(first entry)

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KDYISLNEDLRSWTAADTVAQITQRFYEAEBYABBFRTYLEGECLELLRRYLENGKETLQ 180
EWTTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 141
                                                                                                                                                                                                                                                                                                                              Ovarian tumour marker gene; human; overexpression; upregulation; epithelial tumour; cancer; diagnosis; prognosis; disease monitoring; identification; serous cystadenoma; borderline serous tumour; serous cystadenoma; borderline serous cystadenoma; mucinous cystadenocarcinoma; mucinous cystadenocarcinoma; mucinous cystadenocarcinoma; undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma; adenotirona; Berner tumour; serial analysis of gene expression; SAGE; immune response pathway; cell proliferation regulation; protein folding; membrane localised, secreted; therapeutic target; cytostatic; gene therapy; vaccine.
                                              KDYISLNEDLIKSWTAADTVAQITQRFYEAEBTYABEFRTYLEGECLELLRRYLENGKETLQ
                                                                                                   RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT
                                                                             RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLIWQRDGEEQTQDTELVETRPAGDGT
                                                                                                                                                                                                                                                                                                       HLA-Cw ovarian tumour marker protein, SEQ ID NO:82.
                                                                                                                                                          262 POKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 295
                                                                                                                                  241 FOKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW
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                                                                   EWITGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 120
                                                                                             KDYISLNEDLRSWIAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQ 180
                                          EWTTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 120
  KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQ
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Pred. No. 6
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EGAW/) EGAWA K. (MEDI-) MEDINET 1
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The invention relates to methods for diagnosing and prognosing ovarian tumours in an individual via the detection and measurement of the expression of ovarian tumour marker genes (ARA831812, ARA83180, ARA831812 and ARA83184) or segments thereof (ARA83123-ARA83189, ARA83181 and ARA83183). The methods of the invention are useful for detecting an ovarian tumour in a patient, for identifying an individual at increased risk for developing ovarian cancer, in prognostic tests for assessing the relative severity of ovarian cancer, in tests for monitoring a patient in remission from ovarian cancer and in tests for monitoring disease status in a patient being treated for ovarian cancer. The methods can additionally be used to identify a particular tumour as being an ovarian tumour (1.e., an epithelial ovarian tumour selected from serous cystadenoma, borderline serous tumour, serous cystadenoma,
                                                                                                                                                                                                                                        Detecting and identifying ovarian tumor, identifying increased risk for developing ovarian cancer, and determining effectiveness of ovarian cancer treatment, by measuring expression level of ovarian tumor marker
9
     Hough
     Pizer ES,
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     Morin PJ, Sherman-Baust CA,
                                                                                                         WPI; 2001-626450/72.
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6.6e-250; ö

Mismatches

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Best Loca Matches

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22 61

EWITGYAKANAQIDRVALRNLLRRYNQSEAGSHILQGMAGCDMGPDGRLIRGYHQHAYDG 120

1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 60 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 81

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mucinous cystadenoma, borderline mucinous tumour, mucinous cystadenocarcinoma, endometrioid carcinoma, undifferentiated carcinoma, clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner tumour. The ovarian tumour marker genes of the invention were identified using SAGE (serial analysis of gene expression) and were found to be overexpressed in a broad variety of ovarian epithelial tumour cells relative to normal ovarian epithelial cells. The marker genes are implicated in immune response pathways, in the regulation of cell proliferation and in protein folding, and many of these are membranelocalised or secreted. In addition to their use as diagnostic and
                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                   22 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPRBPWVEQEGPQYW 81
                                                                                                                                                                                                                                                                                                                                                                               GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
                                                                                                                                                                                prognostic markers, the ovarian tumour marker genes or their encoded proteins may be used as therapeutic targets for the treatment and prevention of ovarian cancer. Sequences ABB50257-ABB50259 represent proteins encoded by ovarian tumour marker genes of the invention
                                                                                                                                                                                                                                                                                                                                                Gaps
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100.0%; Pred. No. 6.6e-250;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human diagnostic protein #26717.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG26726 standard; protein; 677 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT;
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2000US-00649167
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Matches 274; Conservative
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N-PSDB; AAS90913.
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                                                                                                                                                                                                                                                                            Sequence 362 AA;
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23-AUG-2000;
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGN) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cutivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in issue, as molecular weight markers and as a food pupplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of layobypeptide and polymucleotide sequences have applications in diagnostics, foremsics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and and can to produce other types of data and products dependent on DNA and anno acid sequences. ABG00010-ABG30377 represent novel human diagnostic maino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from MIPO at the privations.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  331 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      391 EWITGYAKANAQIDRVALRNILRRYNQSEAGSHILQGMNGCDMGFDGRILRGYHQHAYDG
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New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.2%; Score 250; DB 4; Length 677; 100.0%; Pred. No. 4.7e-227; ive 0; Mismatches 0; Indels
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                                                                                                                           Claim 20; SEQ ID NO 57085; 103pp; English.
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Matches 250; Conservative
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                            AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidateric; caequlant; noctropic; vasotropic; antipsoriatic and antiangiogenic. The polymucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polymucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune cills, to treat disorders of haematopoietic cells, autoimmune rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and agonists and antagonists may be also be used in drug screens. AAC7849 to AAC78457 and AAB44240 represent sequences used in the exemplification of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQ 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSHSLRYFSTAVSRPGRGEPRXIAVBYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 87
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                                                                                                                                                                                                                                                                                                              comprising sequences encoding peptides
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allergic reaction, graft versus host disease; organ rejection, haemostatic, thrombolytic, cardiovascular disorder; infection; neurological disease; drug screening.
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                                                                                                                                                                                                                                                                                                              Novel isolated nucleic acids comprising sequenuseful for treating or diagnosing e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 2115-2116; 2352pp; English
                                                                                                                                                   08-MAR-2000; 2000WO-US005882
                                                                                                                                                                             99US-0124270P
                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the present invention
                                                                                                                                                                                                                                        Ruben SM;
                                                                                                                                                                                                                                                                  WPI; 2000-587533/55.
N-PSDB; AAC78195.
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                                                                                         WO200055350-A1
                                                               Homo sapiens
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                                                                                                                     21-SEP-2000,
                                                                                                                                                                                                                                        Rosen CA,
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Best Local 8
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This invention relates to a cancer cell specific HLA-F antigen. The invention includes DNA encoding the antigen, and a method for the used used in a method to diagnose cancer, in which the protein is used to detect anti-HLA-F antibodies in bodily fluids of the patient. The present sequence represents the cancer cell-specific HLA-F antigen of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 İQREYEABBYABBERİYLEGECLELLERYLENGKETLORADPPKAHVAHHPISDHEATLE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer
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78.5%; Score 215; DB 4;
Best Local Similarity 100.0%; Pred. No. 2e-194;
Matches 215; Conservative 0; Mismatches 0
                                                                                                                                                 Human cancer cell specific HLA-F antigen SEQ
                                                                                                                                                                                               HLA-F antigen; cancer cell specific; human
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AAG64619 standard; protein; 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EGAW/) EGAWA K.
(MEDI-) MEDINET KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIMU/) KIMURA K.
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                                                                                                                                                                                                                                                                                                        JP2001095584-A
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                                                                                                 12-SEP-2001
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                                                     AAG64619;
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82 9 120

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                                                                                                                                                                                                                                                           ABP42931 standard; protein; 186
                                                 21-FEB-2000; 2000EP-00200610.
                                                         99US-0122487P
                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                    99; Conservative
                                                                          Dumas Milne Edwards J,
                                                                                   WPI; 2000-500381/45
                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                       N-PSDB; AAC00215
                                                                                                                                                                                    Sequence 120 AA;
           Human; 5' EST;
gene therapy;
                                                                 GEST ) GENSET
                                 EP1033401-A2.
                                                         26-FEB-1999;
                         Homo sapiens
                                                                                                                                                                                                                                                                           22-AUG-2002
                                         06-SEP-2000.
                                                                                                   obtaining
                                                                                                                                                                                                                                                                   ABP42931;
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cardiovascular disorder; respiratory disorder; neurological disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 186 AA;
                                                                                                                                                  WO200200677-A1.
                                                                                                                                                                                     03-JAN-2002.
                                                                                                                                                                                                                                                                                                                                       Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dr primed cDNA libraries. Such ESTs are not well suited for isolating cDNA primed cDNA libraries. Such ESTs are not well suited for isolating cDNA included. S' ESTs are derived from mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cONAs and genomic DNAs. S' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; bifertility; pregrancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorthoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81
                                                         , expressed sequence tag; secreted protein; cDNA isolation; chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 GSHSLRYFSTAVSRPGRGEPRYIAVBYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid that is a 5' expressed sequence tag (5' EST) for inning cDNAs and genomic DNAs that correspond to 5'ESTs and fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; SEQ ID NO 4290; 71pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.1%; Score 99; DB 3; Length 120; 100.0%; Pred. No. 3.3e-85; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 EWITGYAKANAQIDRVALRNILRRYNQSEAGSHILQGMN 99
                                                                                                                                                                                                                                                                                                                                       Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ovarian antigen HPDRT37, SEQ ID NO:4063.
                     Human secreted protein, SEQ ID NO: 4290.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    genomic DNAs that
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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABG54131-ABG56305), and also encompasses polypeptides 90% identical and polymucleotides 95% identical comprising human ovarian antigens to the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigens to polymucleotides, antibodies against human ovarian antigens and the use of ovarian antigens polymucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast cancer, and disorders. Such conditions include ovarian cancer and breast cancer, and disorders (e.g., infertility, disorders origin, reproductive system disorders (e.g., infertility, disorders origin, reproductive system disorders (e.g., chlamydia, HIV, toxoplammensia, endocrine clasorders, infertility, disorders, e.g., mastitis, oophoritis and varian cysts, and dysmenorrhoea), inflammatory conditions (e.g., mastitis, oophoritis and variantis), immune disorders (e.g., congenital and acquired to toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and variantis), immune disorders (e.g., congenital and acquired to the sorders (e.g., anaemia), cardiovascular disorders (e.g., anaemia), cardiovascular disorders and usinary system disorders. Ovarian antigen polypeptides and disorders. Ovarian antigen polypeptides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polymucleotides may be used as food additives or to prepare antibodies (e.g., useful in disease diagnosis, drug targeting and phenotyping. The present sequence enter a human ovarian antigen part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed or the printed or the printed or the printed procession and the sequence data for this patent did netering to the printed processi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 YAKANAQTDRVALRNILRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDGKDYIS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YAKANAQTDRVALRNILRRYNQSBAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDGKDYIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antihody preparation; cytostatic; reproductive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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; Pred. No. 1e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.5%; BCC. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; SEQ ID NO 4063; 2922pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-2000; 2000US-0209467P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-2001; 2001WO-US018569.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen CA;
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hes 70; Conserva
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AAB5849 RESULT

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Consensus sequence of peptides which constitute the alpha-1, alpha-2 and alpha-3 regions of a class I HLA molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New peptide corresp. to major histocompatibility antigen regions - used for modulating cytotoxic T-lymphocyte activity in e.g. transplants or auto-immune diseases.
                                                                                                                                                                                             HLA-A2 epitopes; extracellular domains alpha-1, alpha-2 and alpha-3
                                                                                                                                                                                                                                                                                                                                                                                                  /note= "alpha-3 region"
                                                                                                                                                                                                                                                                                                                    'note= "alpha-1 region"
                                                                                                                                                                                                                                                                                                                                                          "alpha-2 region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clayberger C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                           Location/Qualifiers
AAP80911 standard; protein; 274 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 9; Fig 4; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR12466 standard; protein; 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87US-00008846.
87US-00138547.
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(first entry)
                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                       91. .180
/note= "al
181. .272
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Best Local Similarity 100.
Matches 44; Conservative
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                                                                                (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 274 AA;
                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-DEC-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-1987;
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29-AUG-1991
                                                                            25-MAR-2003
18-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                           WO8805784-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Krensky AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR12466;
                                      AAP80911;
                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                 Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polymucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAB58106 - AAB5848. Lung cancer associated proteins and polymucleotide sequences, their agonists, and antegonists may have neuroprotective; cytostatic; cardioactive; and catagonists may have neuroprotective; cytostatic; cardioactive; and golymucleotide sequences, their agreeological; or antibacterial cativity. The invention also includes antibodies specific for the protein or polymucleotide sequences. The lung cancer associated polymucleotide cor polymucleotide sequences. The lung cancer associated polymucleotide cor polymucleotide sequences. The protein or numerous other diagnostic or research purposes. The proteins may be used to treat disorders such as cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases.

Sequences and proliferative disorders. The proteins may also be used in the course of the invention for the identification and characterisation of the polymucleotide and protein sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                       Human; lung cancer associated protein; neuroprotective; cytostatic; cardicactive; immunoanchilatory; muscular active; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynecological; antibacterial; diagnosis; neural disorder; immune disorder; reproductive; proliferative disorder; wound healing; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 OTODIELVETRPAGDGIFOKWAAVVVPSGEEORYICHVOHEGLP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 ÓTÓDTELVETRPAGDGTPOKWAAVVVPSGEEORYTCHVOHEGLP 75
                                                                                                                                                                                                   Lung cancer associated polypeptide sequence SEQ ID 835.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 16.1%; Score 44; DB 3; I Best Local Similarity 100.0%; Pred. No. 2.2e-33; Matches 44; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 1375; 1425pp; English.
                                                                                AAB58497 standard; protein; 104 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-MAR-2000; 2000WO-US005918.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0124270P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC (ROSE/) ROSEN C A.
                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-587514/55.
N-PSDB; AAF18373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       WO200055180-A2.
                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAR-1999;
                                                                                                                                                               14-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruben SM;
                                                                                                                         AAB58497;
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The concensus sequence is derived from a total of 23 HLA-A,B,C sequences. The protein sequences in the three extrecellular domains (alpha-1, alpha-2 and alpha-3) are shown. The example concerned the effect of peptides from different HLA-A2 epitopes on cytolysis of target cells by CTL of different specificities. (Updated on 25-MAR-2003 to correct FF field.) (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                               16.1%; Score 44; DB 1; Length 274; 100.0%; Pred. No. 4.8e-33; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                            224 QTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 267
                                                                                                                                                                                                                                                                                                                                                                                  224 QTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLA-C exon Cb-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR12466
ID AAR1
XX
AC AAR1
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DT 25-W
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RESULT 10 AAP80911

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polypeptides products for

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The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a mucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer.
                                      New isolated cancer associated nucleic acids and using sera from cancer patients, used to develop diagnosis, monitoring or treatment of cancers.
                                                                                                 Disclosure; Page 417-418; 787pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAO13073 standard; protein; 374 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human polypeptide SEQ ID NO 26965.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-2001; 2001WO-US004927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
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                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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             WPI; 1999-132448/11.
                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAI93004
                                                                                                                                                                                                                                                                                                                                                    Sequence 366 AA;
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                                                                                                                                                                                                                                                                                                                         lung cancer
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                                                                                                                                                                                                                                                                                                                                   Probes comprising part of the DNA sequence encoding the protein can be used to identify Class I genes. The DNA can be expressed for immunisation of animals and prodn. of monoclonal antibodies specific for the HLA-C antigen. See also AAR12465 (same patent) and J03112486 and J03112487. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
Human leukocyte antigen; probe; major histocompatibility complex; MHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                              gene, DNA probe and transformant cells - for immunisation of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 QTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.1%; Score 44; DB 2; Length 366
100.0%; Pred. No. 6e-33;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Breast cancer associated antigen precursor sequence.
                                                                                                                                                                                                                                                                                animals and monoclonal antibody development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY07033 standard; protein; 366 AA
                                                                                                                                                                                                                                                                                                            Claim 4; Page 2; 13pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-00896164.
97US-0061599P.
97US-0061765P.
97US-00948705.
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                                                                                                                                                                                         (OLYU ) OLYMPUS OPTICAL CO LTD
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Obata Y,
                                                                                                                                                                                                                       WPI; 1991-182989/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 366 AA;
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10-OCT-1997;
11-OCT-1997;
22-JUN-1998;
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                                              Homo sapiens
                                                                       JP03112485-A.
                                                                                                                                  22-SEP-1989;
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                                                                                                      14-MAY-1991.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                 Human, cytokine; cell proliferation; cell differentiation, gene therapy; vaccine; peptide therapy, stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; SEQ ID NO 26965; 1399pp + Sequence Listing; English.
16.1%; Score 44; DB 2; Length 366; 100.0%; Pred. No. 6e-33; cive 0; Mismatches 0; Indels
                                             224 QTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 267
                                                             100.0%; Prec. ...
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The invention relates to human polynucleotides (AAI79941-AAI99841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodilatory activity and activity, and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent aid not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                            4; Length 374;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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Best Local Similarity 100.
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                Sequence 374 AA;
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Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
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stem cell proliferation, haematopoiesis, nerve tissue regeneration,
immune suppression, immune stimulation, anti-inflammatory, leukaemia.
                                                                                                                                                                                                                                                                                                                      Novel human secreted protein #3374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-APR-2000; 2000US-00552929.
26-JAN-2001; 2001US-00770160.
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                                                                                                                                                                                                                                                   entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells for use in treatment of a pathology related to aberrant expression physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell
Claim 20; Page 683-684; 765pp; English.
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Search completed: June 18, 2004, 19:29:54 Job time : 63 secs

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proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or retinulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU22510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                     Human; shear stress-response protein; vascular disease; arteriosclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kawabata A, Sakurada K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA sequences, proteins encoded by them and antibodies against 
useful in diagnosis and treatment of vascular disease caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                           Length 380;
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                                                                                                                                                                                                              256 QTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 299
                                                                                                                         16.1%; Score 44; DB 4; Length 380
100.0%; Pred. No. 6.2e-33;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                         Human shear stress-response protein SEQ ID NO: 86.
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100.0%; Pred. No. 2.2e-32;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 60; Page 471-472; 678pp; Japanese.
                                                                                                                                                                                                                                                                                                AAB90793 standard; protein; 120 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99JP-00280976.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-OCT-2000; 2000WO-JP006840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                             (first entry)
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les 43; Conservative
                                                                                                                                         Local Similarity 100.
1es 44; Conservative
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                                                                                               Sequence 380 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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macaca mula

homo sapien homo sapien

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тасаса homod

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Homo sapiens (Human),
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
1-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Nonclassical MHC class I antigen (Fragment).
HIA-F.
                                                                                                                                                                                                                                     324 AA.
                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 274;
                                                                                                                                                                                                                                                01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last seg
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                     PRT;
Q30713
Q95510
Q30711
Q9MY12
Q9MY10
Q9MYH8
Q7YP25
                                                 Q71NY3
Q29645
Q99C1N9
Q8SNC6
Q8MG28
Q8MG20
Q8HWD0
Q951G6
Q29866
Q29866
Q19655
Q860B5
Q30989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.08;
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Query Match
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Q861F0;
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Q861F0
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homo sapien
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macaca mula
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                                           June 18, 2004, 19:27:12; Search time 45 Seconds (without alignments) 1921.155 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                           274
1 GSHSLRYFSTAVSRPGRGEP......QRYTCHVQHEGLPQPLILRW 274
                                                                                                                                                                                                                                                                                                                                                               Description
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Q8wlp5
Q9shc0
Q9shc0
Q9stp8
Q9stp2
Q7yr27
Q860r0
Q9tpx7
Q9tpx7
Q99mx87
Q9mx87
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Q78094
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                                                                                                                                            1017041
      GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                 1017041 segs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                           Post-processing: Listing first 45 summaries
                               - protein search, using sw model
                                                                                                                                                                              SPTREMBL 25:*

1: sparchea:*
2: sp bacrea:*
3: sp_fung:*
4: sp_human:*
5: sp_mammal:*
5: sp_mho:*
6: sp_organelle:*
7: sp_phage:*
                                                                                              OLIGO
Gapop 60.0 , Gapext 60.0
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Q861E9
Q861E9
Q95HC0
Q97E68
Q97E72
Q97E72
Q97E87
Q860E0
Q960E0
Q9MXS7
Q9MXS6
                                                                                                                                                                                                                                                                   sp_virus:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_archeap:*
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Maximum DB seq length: 200000000
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                                                                     US-09-819-371-5
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Match Length
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                               OM protein
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                                                                                  Sequence:
                                                                                                                 Searched:
                                           Run on:
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Result Š Length 324;

DB 7;

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KDYISLNEDLRSWTAADTVAQITQRFYEAEFYAEFRTYLEGECLELLRRYLENGKETLQ 180
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He X., Xu L., Liu Y., Zeng Y.;

He X., Xu L., Liu Y., Zeng Y.;

"Cloning of full-length HLA-F*0101 variant 2 cDNA from Han Chinese.";

submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AF522285, AAM74980.1;

EMBL, AF522289, AAM74982.1;

EMBL, AF522289, AAM74983.1;

EMBL, AF522290, AAM74988.1;

EMBL, AF522291, AAM74988.1;

EMBL, AF522291, AAM74988.1;

EMBL, AF522291, AAM74988.1;

EMBL, AF522291, AAM74889.1;

EMBL, AF522291, AAM74889.1;
                                                                       138 KDYISLNEDLRSWTAADTVAQITQRFYEAEBYAEFFRTYLEGECLELLRRYLENGKETLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Ishitani A., Miki A., Williams L.M., Moore Y., Geraghty D.E.,
"HLA-E, F, and G polymorphism: genomic sequence defines new variation
spanning the nonclassical class I genes.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                            198 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            He X., Liu Y., Xu L., Zeng Y.; "Cloning of full-length HLA-F*0101 variant 1 cDNA from Han Chinese."; Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                  RADPPKAHVAHHPISDHEATLRCWALGFYPABITLTWQRDGEEQTQDTELVETRPAGDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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Pred. No. 3.3e-279;
                                                                                                                                                                                                                                                                       241 FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
                                                                                                                                                                                                                                                                                                              258 FQKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 291
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Pfam; PF00129; MHC I; 1.
Probom; PF00159; MHC I; 1.
PROSTE; PS00225; CRYŠTALLIN BETAGAMMA; 1.
PROSITE; PS00225; CRYŠTALLIN BETAGAMMA; 1.
PROSITE; PS002050; IG LIKE; 1.
PROSITE; PS002090; IG MHC; 1.
SEQUENCE 346 AA; 39051 MH; D4782AA4697;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             346
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01-MAR-2002 (TrEMBLrel. 20, C;
01-MAR-2002 (TrEMBLrel. 20, Le
01-OCT-2003 (TrEMBLrel. 25, Le
MHC class Ib antigen.
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Best Local Similarity
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                                   121
                                                                                                                                                     181
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                                                                                                                                                                                                                61 EWITGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 120
                                                                                                                                                                                                                                                       121 KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQ 180
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                                                                                              GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
                                Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Liu Y., Xu L., Zeng Y., He X.;

Submitted (JAN-2003) to the BMBL/GenBark/DDBJ databases.

Submitted (JAN-2003) to the BMBL/GenBark/DDBJ databases.

BMBL, AV221102; AA034407.1; -.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0006955; P:immune response; IEA.

InterPro; IPR00110; IG-like.

InterPro; IPR00110; IG-like.

InterPro; IPR00139; MG_I.

R Pfam; PP00047; IG, 1.

R Pfam; PP00047; IG, 1.

R PRINTS; PR01538; MGCLASSI.

R SWART; SM00407; IGC.1; 1.

R SWART; SM00407; IGC.1; 1.
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                                   0; Indels
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(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
   100.0%; Pred. No. 3.1e-279; ive 0; Mismatches 0;
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PROSITE; PSS0835; IG LIKE; 1.
PROSITE; PS00290; IG MHC; 1.
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01-JUN-2003 (TrEMBLrel. 24, Crea
01-JUN-2003 (TrEMBLrel. 24, Last
01-OCT-2003 (TrEMBLrel. 25, Last
MHC class I antigen (Fragment).
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Matches 274; Conservative
   al Similarity 100.
274; Conservative
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Best Local
Matches 27
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0861E9
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SEQUENCE FROM N.A.

Ishitani A., Miki. A., Williams L.M., Moore Y., Geraghty D.E.;

Ishitani A., Miki. A., Williams L.M., Moore Y., Geraghty D.E.;

"Hid-E, F., and G polymorphism: genomic sequence defines new variation
repanning the nonclassical class I genes.";

Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

-!-FUNCTION: INVOLVED IN THE PRESENTATION OF POREIGN ANTIGENS TO THE
INMUNE SYSTEM (BY SIMILARITY).

-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

MICROGOBOLOLIN) (BY SIMILARITY).

-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

MICROGOBOLOLIN) (BY SIMILARITY).

EMBL; AF523291; AAM74986.1; -..

BRBL; AF523291; AAM74987.1; -..

RRBL; AF523291; AAM74987.1; -..

RRBL; AF523291; Cintegral to membrane; IEA.

GO; GO:0016021; Cintegral to membrane; IEA.

BRBL; AF503291; AAM74987.1; -..

RRBL; AF503291; AAM7498
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142 KDYISLNEDLRSWTAADTVAQITQRFYEAEEFYAEEFRTYLEGECLELLRRYLENGKETLQ 201
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                                                       RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLITWQRDGEEQTQDTELVETRPAGDGT
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Mammalia; Butharia; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.2%; Score 250; DB 7; L¢
100.0%; Pred. No. 5.6e-254;
ive 0; Mismatches 0;
                                                                                                                                                                                                    262 FQKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 295
                                                                                                                                                                    241 FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
                                                                                                                                                                                                                                                                                                                                                                  346 AA.
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PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00290; IG MHC; 1.
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SEQUENCE 346 AA; 39061 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR01638; WHCCLASSI.
ProDom; PD000050; MHC I; 1.
SMART; SM0407; IGc1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 250; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                ol-OCT-2002 (TrEMBLEE).
01-OCT-2003 (TrEMBLEE).
MHC class Ib antigen.
                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                       120
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                                                                                                                  22 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
                                                                GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
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           Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Lung carcinoma;

Strausbeeg R.;
Strausbeeg R.;
Submitted (JUN-201) to the EMBL/GenBank/DDBJ databases.
EMBL; BC009260; AAH09260.1; --
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:00160955; P:immune response; IEA.
InterPro; IPR0011064; Crystallin.
InterPro; IPR001597; Ig-1.
InterPro; IPR001597; Ig-1.
InterPro; IPR0013006; Ig-MHC.
InterPro; IPR001309; MHC_I.
R Pfam; PF001047; Ig; 1.
R PR001129; MHC I; 1.
R PR001TS; PR001630; MHC_I.
R PROSITE; SW00407; IG-1.
R PROSITE; PS00225; IG-INEE; 1.
R PROSITE; PS00229; IG-INEE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
Similar to major histocompatibility complex, class I, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     442 AA; 50427 MW; 6459D3E5F4B5704A CRC64;
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100.0%; Pred. No. 4.1e-279;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
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           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 274; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI TaxID=9606;
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202 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT 261
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                                                                                                                                                                                                                                              Williams S.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS INMUNE SYSTEM (BY SIMILARITY).

-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).

EMBL, ALO22723; CAB46623.1; -...
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                                                                                                                 Score 250; DB 7; Le
Pred. No. 5.9e-254;
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR001604; Crystallin.
InterPro; IPR00110; IG-like.
InterPro; IPR003006; IG-MC.
InterPro; IPR001309; MHC_I.
Pfam; PF00129; MHC_I:
Pfam; PF00129; MHC_I:
PRINTS; PR01639; MHC_I:
PRODOM; PR000050; MHC_I:
PRODOM; PR000050; MHC_I:
SWART; SW00407; IGG1:
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100.0%; Pred. No. ...
0; Mismatches
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PROSITE; PSS0835; IG LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
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SEQUENCE 362 AA: 40578 M
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Matches 250; Conservative
                                                                                             PRELIMINARY;
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                   FORWAAVVVP 250
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                 Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                         MEDINE-21291697; PubMed-11398964;
Adams E.J., Parham P.;
"Genomic analysis of common chimpanzee major histocompatibility
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                                                                  Last sequence update)
Last annotation update)
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Last annotation update)
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Local Similarity 100.0%; Pred. No. 8.1e-210; les 208; Conservative 0; Mismatches 0;
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Immunogenetics 53:200-208(2001).
EMBL, AR338352, AAK7749:1,.
EMBL, AR338352, AAK7749:1,.
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0016021; C:integral to membrane; IEA.
InterPro; IPR001064; Cryfetallin.
InterPro; IPR001064; Cryfetallin.
InterPro; IPR0010300; IG_IG.
InterPro; IPR001039; MHC_I.
Pfam; PF001029; MHC_I.
Pfam; PF001029; MHC_I.
PR0MT; RF001030; MHC_I.
PR0MT; RF001030; MHC_I.
PR0MT; SM00407; IGC1; I.
PROSITE; PS00205; CRYSTALLIN_BETAGAMMA; I.
PROSITE; PS00220; IG_LIKE; I.
346 AA
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                                              Created)
PRT;
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PRELIMINARY;
                                                                  01-DEC-2001 (TrEMBLr
01-OCT-2003 (TrEMBLr
MHC class I antigen.
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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142 KDYISINEDIRSWTAADTVAQITQRFYEAEBYABEFRIYLEGECLELLRRYLENGKETLO 201

EWTTGYAKANAQTDRVALRNILLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 82 EWITGYAKANAQIDRVALRNILRRYNOSEAGSHILQGWNGCDMGFDGRLLRGYHQHAYDG 121 KDYISLNEDLRSWTAADTVAQITQRFYEAEFYAEFFRTYLEGECLELLRRYLENGKETLQ

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              [1]

SEQUENCE FROM N.A.

MEDLINE=22709134; PubMed=12799463;

Anzai T., Shiina T., Kimura N., Yanagiya K., Kohara S., Shigenari A. Yamagata T., Kulski J.K., Naruse T.K., Fujimori Y., Fukuzumi Y., Yamazaki M., Tashiro H., Iwanoto C., Umohara Y., Imanishi T., Meyer A., Ikeo K., Gojobori T., Bahram S., Inoko H., "Comparative sequencing of human and chimpanzee MHC class I regions unveils insertions/deletions as the major path to genomic
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                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 100:7708-7713(2003).
EMBL, AB100087; BAC78191.1; -.
SEQUENCE 362 Aa; 40625 MW; BA5699D08181AIFF CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI\_TaxID=9606; Created) Last sequence update) Last annotation update) Q860R0; 01-JUN-2003 (TrEMBLrel. 24, Cr 01-JUN-2003 (TrEMBLrel. 24, La 01-OCT-2003 (TrEMBLrel. 25, La MHC class Ib antigen. PRELIMINARY; Homo sapiens (Human) Q860R0 RESULT 9

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Liu Y., He X., Xu L., Zeng Y.;

Liu Y., Yu L., Xu 
87 22 GSHSLRYFSTAVSRPGRGEPRYLAVEYVDDTQFLRFDSDAAIPRMEPREPRWVEQEGPQYW 1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW .; 0 Query Match 66.4%; Score 182; DB 7; Length 254; Best Local Similarity 100.0%; Pred. No. 1.3e-182; Matches 182; Conservative 0; Mismatches 0; Indels

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243 9 1 PPKAHVAHHPISDHEATLRCWALGFYPABITLTWQRDGBEQTQDTBLVETRPAGDGTFQK 184 PPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGTFQK Gorilla gorilla (gorilla). Gorilla gorilla (gorilla). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Gorilla. Momen TaxID=9593; GTRAIN-Shanba;
Grimeley C.;
HIAA-F: A monomorphic locus in an African-American sample.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
BMB1, AF185566; AAD51634.1;
InterPro; IPR00110; Ig-11ke.
InterPro; IPR003597; Ig\_c1.
InterPro; IPR003006; Ig\_MC.
Pfam; PF00047; Ig; 1.
SWART; SM00407; IGC1; 1. 31.8%; Score 87; DB 7; Length 91; 100.0%; Pred. No. 3.9e-83; rive 0; Mismatches 0; Indels 01-WAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
MHC class I antigen (Fragment). 1 Similarity 100. 87; Conservative PRELIMINARY; SEQUENCE FROM N.A. Query Match Best Local Si Matches 87; RESULT 10 Q9TPX7 SO ORRESPONDENT STATE OF STATE ઠ ઠે 셤

nouno saprens unuman). Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. Last sequence update)
Last annotation update) 316 AA 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequenced-2003 (TrEMBLrel. 25, Last sequenced procedin (Fragment). HLA-C. PRT; PRELIMINARY; Homo sapiens (Human) 029958; 029958 RESULT 11
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SEQUENCE FROM N.A. MEDLINE=89122144; PubMed=2914713;

NCBI\_TaxID=9606;

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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.

BEMBL; AY204730; AA084319.1; -.

R GO; GO:00016020; C:membrane; IEA.

R GO; GO:00016020; C:membrane; IEA.

R InterPro; IPR007110; Ig-1ike.

R InterPro; IPR003597; Ig-1.

R InterPro; IPR003597; Ig-1.

R InterPro; IPR003006; Ig, MHC.

R InterPro; IPR004039; MHC.

R Pfam; PF00129; MHC.1.

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Pfam; PF00129; MHC I; 1.
PRINTS; PR01638; MHCI; 1.
PROD10050; MHCI; 1.
SNART; SN00407; 1G01; 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00290; IG MHC; 1.
Glycoprotein; Transmembrane.
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SEQÜENCE 316 AA; 35380 MW; C03B1EC87F75C9BA CRC64;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae;
Carcopithecinae, Macaca.
                                                                                                                                                                                                                                                                                             Query Match 22.6%; Score 62; DB 7; Length 314; Best Local Similarity 100.0%; Pred. No. 2.4e-56; Matches 62; Conservative 0; Mismatches 0; Indels
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SEQUENCE 353 AA; 39448 MW; ECIAOA7DB085F5B7 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
MHC class I heavy chain antigen (Fragment).
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RA WEDLINE-20260999; PubMed=10803844;

RA WEDLINE-20260999; PubMed=10803844;

RA ROWELL T.J., Rojo S., Lopez de Castro J.A., Taurog J.D., Watkins D.I.;

RA Rowell T.J., Rojo S., Lopez de Castro J.A., Taurog J.D., Watkins D.I.;

RT "A high incidence of Shigella-induced arthritis in a primate species:

RT "A high incidence of Shigella-induced arthritis in a primate species:

RT "A high incidence of Shigella-induced arthritis D.I.;

RESPI PROFES OF SIMILARITY).

RESPI PROFESSI D.I. THE PRESENTATION OF FOREIGN ANTICENS TO THE C. IMMUNE SYSTEM (BY SIMILARITY).

REMEL, AFISTAGO, AAP71169.1;

RESPI PROFESSI D.I. THE PRESENTATION OF FOREIGN ANTICENS TO THE C. MICROGLOSI; P.I. THE PROFESSI D.I. THE PROFESSI
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Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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100.0%; Pred. No. 3e-55;
ive 0; Mismatches 0; Indels
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01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
MHC class I heavy chain antigen.
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Last sequence update)
Last annotation update)
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OCT-2000 (TREMBLrel. 15, Last sequence up
OCT-2003 (TrEMBLrel. 25, Last annotation
class I heavy chain antigen (Fragment).
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                             Q 255
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MHC class I }
MAMU-A.
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                                                                                                                                                                                                                                                          O9MXS6;
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Q9MXS5
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Q9MXS6
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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llarity 100.0%; Pred. No. 3.1e-55;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOST Condition of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the
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ne : 46 secs
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PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF157401; AAF71170.1;
HSSP; P30685; 1A9E.
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Pfam; PF00129; MHC I; 1.
PRINTS; PR01638; MHCLASSI.
ProDom: PD000050; MHCLASSI.
SMART; SM00407; IGc1; 1.
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SEQUENCE 365 AA; 40772 M
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P30461 P30462 P30464 P930466 PP30466 PP3989 P18463 P930475 P93

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                                                                                                                                                                                                                                                                                                                                                                           01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
HILA class I histocompatibility antigen, alpha chain F precursor (HLA F antigen) (Leukocyte antigen F) (CDA12).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shina S., Taniya G., Oka A., Inoko H.; 6p21.3 HLA class I region."; Shina S., Taniya G., Oka A., Inoko H.; 6p21.3 HLA class I region."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION. Involved in the presentation of foreign antigens to the immune system.
-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90111605; PubMed=1688605; Geraghty D.E., Wei X., Orr H.T., Koller B.H.; Mei X., Orr H.T., Koller B.H.; Meixocyte antigen F (HLA-F). An expressed HLA gene composed a class I coding sequence linked to a novel transcribed repetitive element.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=91197889; PubMed=1707659;
MEDLINE V. Bpstenn H., Helmes N.;
"The human class I MHC gene HLA-F is expressed in lymphocytes.";
Int. Immunol. 2:531-537(1990).
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EMBL; AP000521; BAB63337.1; -.
PIR; A60384; A60384.
HSSP, Q30201; JA6Z.
Genew; H9020; JA6Z.
MIM; 143110; -.
GO; GO:0030106; F:MHC-Class I receptor activity; TAS.
InterPro; IPR00110; Ig-1ike.
InterPro; IPR003597; Ig-21.
InterPro; IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                         362
1802_PANTR
1803_GORGO
1807_HUMAN
1808_HUMAN
1813_HUMAN
1814_HUMAN
1815_HUMAN
1815_HUMAN
1818_HUMAN
1817_HUMAN
                                                                                                                                                                                  1B38_HUMAN
1B39_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Exp. Med. 171:1-18(1990)
 microglobulin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Human)
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   Homo sapiens
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ID HLAF HUMAN
AC P30511;
   homo sapien
pan troglod
homo sapien
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homo sapien
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P16215 pan troglod
P33617 macaca mula
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                                                                                                                                     June 18, 2004, 19:26:37; Search time 17 Seconds (without alignments) 839.248 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                274
1 GSHSLRYFSTAVSRPGRGEP.....QRYTCHVQHEGLPQPLILRW
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P13747 |
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                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                              141681 segs, 52070155 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
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HLAF MACHU
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HLAH HUMAN
1A01 HUMAN
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1A03 HUMAN
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1A04 PANTR
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1A24 HUMAN
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HLAE HUMAN
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HLAG HUMAN
1C01 GORGO
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GORGO
GORGO
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                                                                                                - protein search, using sw model
                                                                                                                                                                                                                                                                                                        Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CHLA class I histocompatibility antigen, CH28 alpha chain precursor.
                                                                                                                                                                                                            HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN F.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINES 88319000; PubMed=3412467; Jackson A.P., Parham P.; Lawlor D.A., Ward F.E., Ennis P.D., Jackson A.P., Parham P.; "HLA-A and B polymorphisms predate the divergence of humans and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90201944; PubMed=1690682; Lawlor D.A., Warzen E., Ward F.E., Parham P.; "Comparison of class I MHC alleles in humans and apes."; Immunol. Rev. 113:147-185(1990).
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BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (BY
N, B8DD041F820A34E1 CRC64;
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InterPro; IPR001039; WHC_I.
Pfam; PF00042; id; I.
Pfam; PF00129; WHC_I; I.
PRINTS; PR01638; MHCCLIASSI.
ProDom; PD0000505; MHCCLIASSI.
SWART; SM04407; IGCL; I.
PROSITE; PS50835; IG_LIKE; I.
PROSITE; PS00290; IG_MHC; I.
MHC_I; Transmembrane; Glycoprotein; Signal.
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                40568 MW;
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Conservative C
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Nature 335:268-271(1988)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        362 AA;
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Best Local Simil
Matches 274; C
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P16215;
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DOMAIN
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CARBOHYD
SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 TTGYAKANAQTDRVALRNILBRYNQSBAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDGKD 122
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to the
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CH28 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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                         immune system.
-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
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Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
FUNCTION: Involved in the presentation of foreign antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 346;
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BY SIMILARITY.

N-LINKED (GLCNAC. . .) (B)

F83E882D5C2E0971 CRC64;
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100.0%; Pred. No. 3.4e-124;
ive 0; Mismatches 0;
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01-FEB-1994 (Rel. 28, Last sequence update)
15-JUJ-1999 (Rel. 38, Last annotation update)
HIA Class I histocompatibility antigen, alpha
HIA-P OR HIAP.
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                                                                                                                                                                                                                                                                                                EMBL; M30685; AAA87973.1; -...
HSSP; Q30201; LA6Z.
INTERPRO; IPR007100; 199-like.
INTERPRO; IPR0013597; 19_-like.
INTERPRO; IPR001399; MHC_I.
Pfam; PP00147; 19_I.
Pfam; PP00129; MHC_I.
PRINTS; PR01658; MHC_I.
PRODO; PR00189; MHC_I.
PRODO; PR00189; MHC_I.
PRODO; PR00189; MHC_I.
PRODO; PR00189; MHC_I.
NART; SW0407; IGLI.
PROSITE; PS50835; IG_LIKE; 1.
MHC I; Transmembrane; Glycoprote
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Best Local Similarity 100.
Matches 126; Conservative
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346 AA;
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                                                                    microglobulin)
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P33617;
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DOMAIN
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HLAF MACMU
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                  MEDLINE-82151002; PubMed-6461010; Malissen M., Malissen B., Jordan B.R.; malissen m., malissen B., 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC TAIL.
N-LINKED (GLCNAC. . .) (BY SIMILARITY).
                                                                                                                           Proc. Vatl. Acad. Sci. U.S.A. 79:893-897 (1982).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM. COULD BE THE PRODUCT OF A PSEUDOGENE.
-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
CXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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P30443; O77964; O78171; O9MYA3; O9TP25; O9TOP5;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
HLA class I histocompatibility antigen, A-1 alpha chain precursor (MHC class I antigen A*1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.1%; Score 44; DB 1; Length 362; 100.0%; Pred. No. 3.9e-38; ive 0; Mismatches 0; Indels
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MINI, 142800; -..

MINI, 142800; -..

GO; GO:0005887; C:integral to plasma membrane; NAS.

GO; GO:000505; P:immune response; NAS.

GO; GO:000106; F:immune response; NAS.

InterPro; IPR003597; Ig-11ke.

InterPro; IPR003069; Ig-NHC.

R InterPro; IPR003009; MHC_I:

R Pfam; PP0047; ig: 1.

R PF0047; ig: 1.

R PT0017; ig
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OBCDAE9D61A81B86 CRC64;
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HSSP; P03989; 1HSA.
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Matches 44; Conservative
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                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                       of HLA-F.";
Immunogenetics 38:141-145(1993).
-!- FUNCTION: Involved in the presentation of foreign antigens to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                               immune system.
-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).
[1]
SEQUENCE FROM N.A.
MEDLINE=93246295; PubMed=8482576;
Otting N., Bontrop R.E.;
"Characterization of the rhesus macaque (Macaca mulatta) equivalent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
(1)
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01-ARR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
HIA class latocompatibility antigen, alpha chain H precursor (HIA-AR) (HIA-12.4).
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39300 MW;
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1es 59; Conservative
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P01893;
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GO; GO:0005887; C:integral to plasma membrane; NAS. GO; GO:0030106; F:MHC class I receptor activity; NAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR007110; Ig-11ke.
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EMBL;
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     NECUREDER S. PubMed=12477932;

Characher R. D., Collins F. S., Wagner L., Shenmen C.M., Schuler G.D., Rianser R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Datchenko. L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheez B. B. Batchenko. L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheez T.E., Braplecon M. Scarse M.B., Bonaldo M.F., Casavant T.L., Scheez T.E., Arable S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gibbs R.A., Acharis S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Tanky J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Miting M., Madan A., Young A.C., Shevchenko Y., Bonifard G.G., Alakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Albertiquez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E., Jones S.J.M., Marra M.A.; Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Froc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                             SEQUENCE FROM N.A. (A*0101).
MEDLINE=88234547; PubMed=3375250;
Parham P., Lomen C.E., Lawlor D.A., Ways J.P., Holmes N., Coppin H.L.,
Salter R.D., Wan A.M., Ennis P.D.;
"Nature of polymorphism in HIA-A, -B, and -C molecules.";
Proc. Natl. Acad. Sci. U.S.A. 85:4005-4009(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (A*0101).
MEDLINE=98007773; PubMed=9349617;
Laforet M., Froelich N., Parissiadis A., Pfeiffer B., Schell A.,
Faller B., Woehl-Jaegle M.L., Cazenave J.P., Tongio M.M.;
"A nucleotide insertion in exon 4 is responsible for the absence of expression of an HLA-A*01 allele.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95282145; PubMed=7761977;
Browning M.J., Madrigal J.A., Krausa P., Kowalski H.,
Allsopp C.E., Little A.-M., Turner S., Adams E.J., Arnett K.L.,
Bodmer W.F., Partam P.;
"The HLA-A.B. C genotype of the class I negative cell line Daudi
reveals novel HLA-A and -B alleles.";
Tissue Antigens 45:177-187(1995).
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MEDLINE=98101100, PubMed=9438203;
Sitha S., Scheltinga S.A., Johnston-Dow L.A., White C.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (A*0101). Warsh S.G.E.; Waller M.J., Robinson J., Marsh S.G.E.; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                           Warren E.;
Submitted (APR-1989) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                             SEQUENCE FROM N.A. (A*0101).

MEDLINE=89235215; PubMed=2715640;

Parham P., Lawlor D.A., Lowen C.E., Ennis P.D.;

Parham P., Lawlor D.A., Lowen C.E., Ennis P.D.;

Tilyersty and diversification of HLA-A,B,C alleles.";

J. Immunol. 142:3937-3950(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Girdlestone J.;
"Nucleotide sequence of an HLA-Al gene.";
Nucleic Acids Res. 18:6701-6701(1990).
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MEDLINE=91067475; PubMed=2251137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .ssue Antigens 50:347-350(1997).
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TISSUE=Brain;
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NCBI_TaxID=9606;
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          der van Zwan A.W., Bakema J.B., Rozemuller B.H., van der Tweel J.G.,
Kronink M.N., Tilanus M.G.J.;
"A generic sequencing based typing approach for the identification of
HLA-A diversity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=88088800; PubMed=3121736;
Sant A.J., Zacheis M., Rumbarger T., Giacoletto K.S., Schwartz B.D.;
"Human Ia alpha- and beta-chains are sulfated.";
J. Immunol. 140:155-160(1988).
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-!- PTM: Sulfated.
-!- PTM: Sulfated.
-!- POLYMORPHISM: The following alleles of A-1 are known: A*0101, A*0102, A*0103, A*0106 and A*0107. The sequence shown is that of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
., Bakema J.E., Rozemuller E.H., van der Tweel J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 26-206 FROM N.A. (A*0106).
MEDLINE=20309230; PubMed=10852390;
Ellis J., Steiner N.K., Kosman C., Henson V., Mitton W., Koester Ny J., Hartzman R.J., Hurley C.K.;
"Seventeen more novel HiA-A locus alleles.";
Tissue Antigens 55:369-373(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEGUENCE OF 26-206 FROM N.A. (A*0107).
Tamouza R., Fortier C., Mahfoudh N., Schaeffer V., Poirier J.C., Marzais F., Gautreau C., Charron D.;
Marzais F., Gautlell.",
"A new HibA-A*01 allell.",
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                              TISSUE=Blood,
MEDLINE=21100775; PubMed=11182232;
MEDLINE=21100775; PubMed=11182232;
Poland G.A., Sohni Y., Domanico M., Kroning C.M., DeGoey S.R.,
Jimale M., Jacobson R.M., Moore S.B.;
"High frequency of HLA-A*0103 allele in a Somali population.";
Hum. Immunol. 62:197-200(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the immune system.
                                                                                                                                                                                                  SEQUENCE OF 26-206 FROM N.A. (A*0103).
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EMBL; AF143232; AAD33894.1; --
EMBL, AF142331; AAD33894.1; JOINED.
EMBL; AF219633; AAF73862.1; JOINED.
EMBL; AF219632; AAF73862.1; JOINED.
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EMBL, X5710; CAA39243.1; -
EMBL, 293949; CAB07989.1; -
EMBL, AJ278305; CAB93537.1; -
                                                                                                                  Hum. Immunol. 57:120-128(1997).
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Y12469; CAA73072.1; -.
Y12470; CAA73073.1; -.
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MIM; 142800; -.
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PIR, 161856; 161856.
HSSP; 019673; 1HSB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN
-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FC452786BD038D3E CRC64;
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P04339; 019546; 019756; 09GJE6; 09GJE7; 09GJE8; Q9MYG4; Q9TPR8;
13.4UG-1987 (Rel. 05, Created)
10.0CT-2003 (Rel. 42, Last sequence update)
110.0CT-2003 (Rel. 42, Last annotation update)
111.0CT-2003 (Rel. 42, Last annotation update)
11.0CT-2003 (Rel. 42, Last annotation update)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE-64207948; PubMed-6609814; Strachan B.R.; Strachan T., Sodoyer R., Damotte M., Jordan B.R.; Micomplete nucleotide sequence of a functional class I HLA gene, HLA-A3: implications for the evolution of HLA genes."; EMBO J. 3:887-894(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.1%; Score 44; DB 1; Length 365; 100.0%; Pred. No. 3.9e-38; ive 0; Mismatches 0; Indels
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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Ellexson M.E., Hildebrand W.H.;
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44; Conservative
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115 22
207 22
209 3
309 3
333 125 11
227 227 110 110 110 1365 AA;
                                 microglobulin).
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TRANSMEM
DOMAIN
DISULFID
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Lawlor D.A., Warren E., Ward F.E., Parham P.;
"Comparison of class I MHC alleles in humans and apes.";
Immunol. Rev. 113:147-168(1990).
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Pram; PRO047; 19; 1.
Pram; PRO047; 19; 1.
PRINTS; PRO1638; MHCC1ASI.
PRODON; PRO167; 10:
SMART; SMO407; 10:
PROSITE; PS00290; 1G_MHC; 1.
PROSITE; PS00290; 1G_MHC; 1.
PROSITE; PS00290; 1G_MHC; 1.
24
CHAIN
25 365 HLA CLASS I HISTOCCOMPATIBILITY ANTIGEN,
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SULFATION (POTENTIAL).
N-LINKED (GLCNAC. ..) (BY SIMILARITY).
BY SIMILARITY.
F -> S (in allale A*0102).
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1993 (Rel. 25, Last amotation update)
01-APR-1993 (Rel. 25, Last amotation update)
01-APR-1993 (Rel. 25, Last amotation update)
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.

NCBI_TaxID=9598;
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FTIG=VAR 004332.

FTIG=VAR 004332.

FTIG=VAR 004332.

G-> R (in allele A*0102).

FTIG=VAR 016720.

FTIG=VAR 016720.

FTIG=VAR 016720.

FTIG=VAR 016720.

FTIG=VAR 016721.

FTIG=VAR 016723.

FTIG=VAR 016723.

FTIG=VAR 016723.

FTIG=VAR 016723.
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8667AFF3F06C4932 CRC64;
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     InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR001039; MHC_I.
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MEDLINES-99180630; PubMed=10079303;
Santos S., Balas A., Garcia-Sanchez F., Lillo R., Merino J.L.,
Vicario J.L.;
"Complete cDNA coding sequence of a new HLA-A3 subtype (A*0304) with a
new HLA polymorphism at exon 3.";
Immunogenetics 49:360-361(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  microglobulin).
SUBCELLULAR LOCATION: Type I membrane protein.
POLYMORPHISM: The following alleles of A-3 are known: A*0301
(A-3.1), A*0302, A*0304 and A*0305. The sequence shown is that of A*0301.
                                                      SEQUENCE FROM N.A. (A*0301).
Shilina S., Tamiya G., Oka A., Inoko H.;
"Homo sapiens 2.99,817bp genomic DNA of 6p21.3 HLA class I region.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                   SEQUENCE FROM N.A. (A*0302).
MEDLINE=85290811;
DOWAN E.P., Jordan B.P., Coligan J.E.;
"Molecular cloning and DNA sequence analysis of genes encoding cytotoxic T lymphocyte-defined HiA-A3 subtypes: the E1 subtype.";
J. Immunol. 135:2835-2841(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Poli F., Frison S., Crespiatico L., Longhi E.;
"Identification of a HLA-A*03 new variant.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Involved in the presentation of foreign antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 26-206 FROM N.A. (A*0305).
Becher M.P., Wu J., Williams T.,
"Novel human HLA-A alleles identified in potential bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the immune system.
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (A*0302).
Bettinotti M.P., Hadzikadic L., Adams S., Marincola F.M.;
"Complete coding sequence of HAA-A*0302.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
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GO: 0005887; C:integral to plasma membrane; NAS.
GO: 001010106; F:MHC class I receptor activity; NAS.
GO: 001006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, X00492, CAA25162.1, ALT_SEQ.
EMBL, U32184; AAB63980.1;
EMBL, AP000519; BAB63400.1;
EMBL, AP000519; BAB63400.1;
EMBL, AF01561; AAF28734.1;
EMBL, AF015930; AAB6682.1;
EMBL, AF190719; AAF603243.1;
EMBL, AF190719; AAF60364.1;
EMBL, AJ401086; CAC06086.1;
EMBL, AJ401086; CAC06086.1;
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MIM; 142800; -.
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HSSP; O19673; 1HSB.
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TRANGE BERKER BE

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-!- FUNCTION: Involved in the presentation of foreign antigens to the
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01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CHLA class I histocompatibility antigen, A-108 alpha chain precursor.
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-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Cararrhini, Hominidae, Pan.
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InterPro; IRR003557; Ig_c1...
InterPro; IRR003057; Ig_c1...
InterPro; IRR003005; Ig_MHC.
InterPro; IRR001039; MHC_I.
Pfam; PR00047; Ig_1...
Pfam; PR00129; MHC_I; 1.
Pr000m; PR000500; MHC_I; 1.
Pr000m; PR000050; MHC_I; 1.
SNART; SM00407; IG_LIKE; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
IMHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
SIGNAL
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Mayer W.E., Jonker M., Klein D.; Ivanyi P., van Seventer G.
Klein J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.1%; Score 44; DB 1; Length 365; 100.0%; Pred. No. 3.9e-38; tive 0; Mismatches 0; Indels
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BY SIMILARITY.

E - V (in allele A*0302).

FTIG=VAR 004351.

L - Q (in allele A*0302).

FTIG=VAR 004352.

D - E (in allele A*0305).

FTIG=VAR 016604.

G -> R (in allele A*0304).

FTIG=VAR 016605.

FTIG=VAR 016605.

W, DEDFCEC4450E0580 CRC64;
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EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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or send an email to license@isb-sib.ch)
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                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBO J. 7:2765-2774 (1988).
-!- FUNCTION: Involved in the presentation of foreign antigens to the
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P13749;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CHLA class I histocompatibility antigen, A-126 alpha chain precursor.
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A-108 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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MEDLINE=89030641; PubMed=2460344;
Mayer W.E., Jonker M., Klein D., Ivanyi P., van Seventer G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 365;
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BY SIMILARITY.

N-LINKED (GLCNAC. . .) (B)

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  modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                          PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
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                                                                         EMBL; X13113; CAA31505.1; ALT_INIT.
PIR; S03535; S03535.
                                                                                                            HSSP, O19673, IHSB.
InterPro; IPR007110; I9-like.
InterPro; IPR003597; I9-like.
InterPro; IPR001039; MHC_I.
Pfam; PP00047; ig; IPFam; PP00129; MHC_I.
Pfam; PP00129; MHC_I.
ProDom; PR00050; MHC_I.
ProDom; PR00050; MHC_I.
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SEQUENCE
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"Nucleotide sequences of chimpanzee MHC class I alleles: evidence for trans-species mode of evolution.";
EMBO J. 7:2765-2774(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                    CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .) (BY SIMILARITY).
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HLA-All split antigens, All.1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1A11 HUMAN STANDARD; PRT; 365 AA.
P13746; 019605; 019606; 029747; 029835; 09BCN0; 09MXI5; 09TQE9;
P13746; 019605; 019606; 029747; 029835; 09BCN0; 09TQPT;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
110-0CT-2003 (Rel. 42, Last annotation update)
HIAA class I histocompatibility antigen, A-11 alpha chain precursor HIAA-A OR HLAAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Klein J.;
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MEDLINE-94287401; PubMed-8016845;
Lin L., Tokunaga K., Ishikawa Y., Bannai M., Kashiwase K.,
Kuwata S., Akaza T., Tadokoro K., Shibata Y., Ouji T.;
"Sequence analysis of serological HLA-All split antigens, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           th 16.1%; Score 44; DB 1; Length 365; Similarity 100.0%; Pred. No. 3.9e-38; 44; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267
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D3C9A810B22A768F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 QIQDIELVETRPAGDGTFQKWAAVVVPSGEEQRYICHVQHEGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTODIELVETRPAGDGIFOKWAAVVVPSGEEORYICHVOHEGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                        A-126 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                Glycoprotein; Signal.
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MEDLINE=89030641; Pubmed=2460344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 26-365 FROM N.A. (A*1101).
                                         HSSP, 019673; IHSB.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003106; Ig C1.
InterPro; IPR003006; Ig MHC.
InterPro; IPR001039; MHC_I.
PEam; PP001047; ig; I.
PEAM; PP001029; MHC_I; I.
PRINTS; PR01059; MHC_I; I.
RNINTS; PR01059; MHC_I, I.
RNINTS; PR01059; MHC_I, I.
RNART; SM00407; IGCI, I.
RNOSITE; PS50835; IG_LIKE; I.
RNOSITE; PS02309; IG_MHC; I.
MHC I; Transmembrane; Glycoprofe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ssue Antigens 43:78-82(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40656 MW;
ZMBL; X13114; CAA31506.1;
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                        PIR; S01171; S0117:
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BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

S -> SGGEGVK (in isoform 2).

FTId=VSP 008099.

E -> K (in allele A*1102).

FTYd=VAR 016731.

K -> E (in allele A*1107).

FTY d=VAR 016731.

K -> E (in allele A*1105).

FTY d=VAR 016731.

K -> E (in allele A*1103).

FTY d=VAR 016733.

F -> E (in allele A*1103).

FTY d=VAR 016733.

FTY d=VAR 016733.

FTY d=VAR 016734.

FTY d=VAR 016734.

FTY d=VAR 016734.

FTY d=VAR 016734.
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R GO; GO:0005897; C:integral to plasma membrane; NAS.

R GO; GO:00010106; F:MHC class I receptor activity; NAS.

R GO; GO:00010106; F:MHC class I receptor activity; NAS.

R InterPro; IPR001109; Ig-11ke.

R InterPro; IPR0013006; Ig-MHC.

R InterPro; IPR001309; MHC_I.

R Pfam; PF00129; MHC_I.

R PFam; PF00129; MHC_I.

R PRINTS; PR01638; MHC_LASSI.

R PRNDOM; PD0000505; MHC_I.

R PRNDOM; PD0000505; MHC_I.

R PROSITE; PS00290; IG_ILKE; I.

R PROSITE; PS00290; IG_ILKE; I.

R MRCITE; RS00290; IG_ILKE; I.

R MRCITE; PS00290; IG_ILKE; I.
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF030910; AAB87052.1; EMBL; AF030909; AAB87052.1; EMBL; AF030909; AAB87052.1; GMBL; AF030909; AAB87052.1; GMBL; A7308097; AAB87051.1; JOINED. EMBL; A730807; AAB87051.1; GMBL; A74455; AAD33991.1; SMBL; AF147454; AAD33991.1; JOINED. EMBL; AF147454; AAD33991.1; JOINED. EMBL; AF165065; AAF25781.1; SMBL; A87083; A8725781.1; SMBL; A87083; A
                                                                                                                                       EMBL, X13111, CAA31503.1, --
EMBL, X1312, CAA31504.1, --
EMBL, D16841, BAA04117.1, --
EMBL, D16842, BAA04118.1, --
EMBL, M16010, AAA65449.1, --
EMBL, M16007, AAA65449.1, JOINED.
EMBL, M16009, AAA65449.1, JOINED.
EMBL, Y17224, CAB38056.1, --
EMBL, X71224, CAB38056.1, --
EMBL, X91399, CAA62745.1, --
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SIGNAL
CHAIN
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EMBL;
EMBL;
EMBL;
         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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"A unique second donor splice site in the intron 5 sequence of the HLA-*il alleles results in a class I transcript encoding a molecule with an elongated cytroplasmic domain.";
Tissue Antigens 55:422-428(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 26-206 FROM N.A. (A*1105).
MEDLINE=20309230; PubMed=10852390;
Blis J., Steiner N.K., Koeman C., Henson V., Mitton W., Koester R., Ng J., Hartzman R.J., Hurley C.K.;
"Seventeen more novel HLA-A locus alleles.";
Tissue Antigens 55:369-373(2000).
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IsoId=P13746-2; Sequence=VSP_08099;
Note=Only produced by allele A*1103;
POLYMORPHISM: The following alleles of A-11 are known: A*1101
(A-11E), A*1102 (A-11K), A*1103, A*1104, A*1105 and A*1107. The sequence shown is that of A*1101.
MEDLINE-87192928; PubMed=2437024;

Cowan E.P., Jelachich M.L., Biddison W.E., Coligan J.E.;

"DNA sequence of HiA-All: remarkable homology with HiA-A3 allows

identification of residues involved in epitopes recognized by

antibodies and T cells.";

Immunogenetics 25:241-250(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (A*1105).
MEDLINE=9932103; PubMed=10395112;
Mortell G., Whalley J., Stewart A., Day S., Lewis L., Makar Y.,
Ross J., Dunn P.P.;
"Identification of an HIA-All serological variant and its
characterization by sequencing based typing.";
Tissue Antigens 53:591-594(1999).
                                                                                                                                                                                                                                       Tijssen H.J., Sistermans B.A., van den Beucken M.J.G., Krausa
Joosten I.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 26-206 FROW N.A. (A*1104).
Chandanayingyong D., Sirikong M., Luangtrakool K., Srinak
Rungroung E., Bejchandra S.;
"All alleles (A*1104).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bettinotti M.P.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                      "Complete sequence analysis of the A*1103 allele."; Tissue Antigens 55:68-70(2000).
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 2) (A*1103).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21561663; PubMed=11703829;
Pyo C.W., Choi H.B., Han H., Hong Y.S.
"Identification of HLA-A*11 variant (A
                                                                                                                                                                                              TISSUE=Blood;
MEDLINE=20166353; PubMed=10703613;
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20340071; PubMed=10885562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (A*1104).
                                                                                                                                                                          FROM N.A. (A*1103).
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                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Blood
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SEQUENCE FROM N.A. (A*2301).
MEDLINE=92104637; PubMed=1729171;
Little A.-M., Madrigal J.A., Parham P.;
Little A.-M., Madrigal J.A., Parham P.;
"Molecular definition of an elusive third HLA-A9 molecule: HLA-A9.3.";
"Molecular definition of an elusive third HLA-A9 molecule: HLA-A9.3.";
Immunogenetics 35:41-45(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Seven novel HLA-A alleles carry previously observed polymorphisms.";
Tissue Antigens 56:551-552(2000).
-:- FUNCTION: Involved in the presentation of foreign antigens to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- SUBCELLULAR LOCATION: Type I membrane protein.
-:- POLYMORPHISM: The following alleles of A-23 are known: A*2301, A*2302, A*2303, A*2304 and A*2305. The sequence shown is that of A*2301.
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .i- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1A23 HUMAN STANDARD, PRT; 365 AA.
P30447; QSTQF1; QSTQF8; QSTQG5; QSTQM6;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
HLA class I histocompatibility antigen, A-23 alpha chain precursor (MHC class I antigen A*23) (A-9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20309230; PubMeda10852390;
Ellis J., Steiner N.K., Kosman C., Henson V., Mitton W., Koester
Ng J., Hartzman R.J., Hurley C.K.;
"Seventeen more novel HiA-A locus alleles.";
Tissue Antigens 55:369-373(2000).
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Hurley C.K.;
                                                                                                                                     Length 365;
                                                                                                                                                                                                                                                                224 OTODIELVETRPAGDGTFOKWAAVVVPSGEEORYTCHVOHEGLP 267
                                                                                                                                                                                                                                                                                                                               248 ÓTÓDTELVETRPAGDGTFOKWAAVVVPSGEEORYTCHVOHEGLP 291
                                                                                                                                                                                                    0; Indels
       T -> S (in allele A*1105).
                                   FIId=VAR 016736.
FE449CEZD4BF6CC5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 26-206 FROM N.A. (A*2304 AND A*2305). MEDLINE=21068830; PubMed=11169246;
                                                                                                                                 16.1%; Score 44; DB 1; Le 100.0%; Pred. No. 3.9e-38; trive 0; Mismatchés 0;
                                   /FTIG=VAR
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EMBL; AR137079; AAD33736.1; JOINED.
EMBL; AR102572; AAD28171.1; JOINED.
EMBL; AR135549; AAD2217.1; JOINED.
EMBL; AR135549; AAD2272.1; ...
EMBL; AR136549; AAD31878.1; JOINED.
EMBL; AR140860; AAD31878.1; JOINED.
                                                                  40937 MW;
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                                                                                                                                                                 Best Local Similarity 100.
       345
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                                                                         365 AA;
       345
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                                                                         SECUENCE
                                                                                                                                        Query Match
       VARIANT
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N-LINKED (GLCNAC. . .) (BY SIMILARITY).
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1A24 HUMAN STANDARD; PRT; 365 AA.
105534; P30448; P30449; Q29908; Q29910; Q95355;
P05534; P30448; P30449; Q29908; Q29910; Q95355;
P0-NOV-1998 (Rel. 09, Created)
10-NOV-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR class I histocompatibility antigen, A-24 alpha chain precursor (MHC class I antigen A*24) (Aw-24) (A-9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N'Guyen C., Sodoyer R., Trucy J., Strachan T., Jordan B.R.; "The HLA-AW24 gene: sequence, surroundings and comparison with the HLA-A2 and HLA-A3 genes."; Immunogenetics 21:479-489(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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            DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig_c1.

DR InterPro; IPR003597; Ig_c1.

DR InterPro; IPR001399; MHC_I.

DR Ffam; PF00047; ig; 1.

DR PEAM; PR00129; MHC_I; 1.

DR PRINTS; PR01638; MHC_I.

DR PRINTS; PR001638; MHC_I.

DR PRINTS; PR001638; MHC_I.

DR PROSITE; PS50835; IG_LIKE; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

DR PROSITE; PS0835; IG_MHC_I.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y -> C (in allele A*2305).
/Frid=VAR 016606.
K -> N (in allele A*2303).
/Frid=VAR 016607.
L -> W (in allele A*2302).
/Frid=VAR 016608.
DG -> EW (in allele A*2304).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         224 QTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 QTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTId=VAR 016609.
C372DE503BF393D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 A-23 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44; DB 1; Lo
Pred. No. 3.9e-38;
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100.0%; Pred. No. ...
... 0; Mismatches
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SEQUENCE FROM N.A. (A*2402 AND A*2403)
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MEDLINE=85206128; PubMed=2987115;
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HGNC:4931; HLA-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191
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les 44; Conserv
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     Genew; HGNC:4
MIM; 142800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jordan B.R.;
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TRANSMEM
DOMAIN
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1A24 HUMAN
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Matches
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CYTOPLASMIC TAIL.
N-LINKED GELCHAC. . .) (BY SIMILARITY).
SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A -- G (in allele A*2401).

| FTIG=VAR 004554.
|-- G (in allele A*2408).
| FTIG=VAR 004356.
| E -- G (in allele A*2408).
| FTIG=VAR 004356.
| G -- R (in allele A*2408).
| FTIG=VAR 004356.
| A -- V (in allele A*2414).
| FTIG=VAR 015765.
| M -- R (in allele A*2414).
| FTIG=VAR 015765.
| FTIG=VAR 015765.
| FTIG=VAR 015766.
| FTIG=VAR 015766.
| G -- N (in allele A*2414).
| FTIG=VAR 015767.
| FTIG=VAR 015769.
                                                                                                                                                                                                                                                                                                                    Glycoprotein; Signal; Polymorphism
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-> R (in allele A*2410).
FTIG=VAR_015770.
                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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EMBL; U18987; AAB60651.1; JOINED.
PIR; I54416; I54416.
RSP; Q95352; IHHK.
Genew; HGNC:4931; HLA-A.
MIM; 142800;
                                                                                        NIM; 142800; ...
Interpro; IPR007111; Ig-like.
Interpro; IPR003597; Ig_cl.
Interpro; IPR003597; Ig_cl.
Interpro; IPR00306; Ig_MHC.
Interpro; IPR001039; MHC_I.
Pfam; PF00129; MHC_I:
Pfam; PF00129; MHC_I:
PRNINTS; PR01648; MHCCLASSI.
PRODOM; PD000050; MHC_I:
PROSITE; PS00085; IG_LIKE; I.
PROSITE; PS00290; IG_MHC; I.
MHC I; Transmembrane; Glycoprote
                                                                                                                                                                                                                                                                                                                                                                                                                    206
2298
3332
345
1110
283
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        В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUB-Blood;

MEDLINE-9741771; PubMed-9271829;

A Gao X., Lester S., Matheacan B., Boettcher B., McCluskey J.;

Gao X., Lester S., Matheacan B., Boettcher B., McCluskey J.;

Tissue Antigens 50:192-196(1997).

-!- FUNCTION: Involved in the presentation of foreign antigens to the immune system.

-!- FUNCTION: Involved in the presentation of foreign antigens to committee and a part of an alpha chain and a beta chain (beta-2-microglobulin).

-!- SUBGNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).

-!- FOLYMORPHISM: The following alleles of A-24 are known: A*2401, A*2402, A*2402, A*2403, A*2406, A*2408, A*2401, A*2413 are found in major racial groups. Allele A*2406 and allele A*2413 are found in the Australian Aborigenal population. Allele A*2414 is found in the Australian Aborigenal population. Allele A*2414 is found in the Australian Aborigenal population. Allele A*2414 is found in the Australian Aborigenal population. Allele A*2414 is found in the Australian Aborigenal population. Allele A*2414 is found in the Australian Aborigenal and descent. The sequence shown is that
    MEDLINE=92104637; PubMed=1729171;
Little A. M., Madrigal J.A., Parham P.;
"Molecular definition of an elusive third HLA-A9 molecule: HLA-A9.3.";
Immunogenetics 35:41-45(1992).
                                                                                                                                                                                                                                                                                                                            ద
                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (A*2402).
MEDLINE=98007772; PubMed=9349616;
Laforet M., Froelich N., Parissiadis A., Bausinger H., Pfeiffer B., Tongio M.M.;
"An intronic mutation responsible for a low level of expression of a HLA-A*24 allele.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97161044; PubMed=9008316;
Gao X., Matheson B.;
"A novel HLA-A*24 (A*2410) identified in a Javanese population.";
Tissue Antigens 48:711-713(1996).
                                                                                                                         MEDLINE=92269955; PubMed=1317015; Belich W.H., Zemmour J., Williams R.C., Luz R., Petzl-Erler M.L., Parham P.; "Untsual HiA-B alleles in two tribes of Brazilian Indians.";
                                                                                                                                                                                                                                                                                                                                                                                                                                     Kashiwase K., Tokunaga K., Ishikawa Y., Qiu L., Furuya M., Sawanaka K., Akaza T., Tadokoro K., Juji T.; "A new A9 sequence HLA-A9HH from Japanese."; MHC 3:9-14(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 26-206 FROM N.A. (A*2406; A*2413 AND A*2414).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 26-206 FROM N.A. (A*2410).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA83264.1; JOINED.
AAA83265.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                  Lissue Antigens 50:340-346(1997)
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EMBL; M64740; AAA5960.1; -.
EMBL; M64741; AAA59601.1; -.
EMBL; Z7342; CAA96512.1; -.
EMBL; D83516; BAA11936.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (A*2408).
                                                                                                          SEQUENCE FROM N.A. (A*2402)
                                                                                                                                                                                                         Nature 357:326-329(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U37110; U37113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of A*2402
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                                                                                      Length 365;
                                                                                                                                                                      224 QIQDTELVETRPAGDGTFQKMAAVVVPSGEEQRYTCHVQHEGLP 267
                                                                                                                                                                                              248 ÇIQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYICHVQHEGLP 291
                                                                                                                                0; Indels
206 206 T -> A (in allele A*2401).
/FTId=VAR 004360.
365 AA; 40688 MW; D33684D126F98EC3 CRC64;
                                                                                    Query Match
16.1%; Score 44; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 3.9e-38;
Matches 44; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                    1730 HUMAN STANDARD; PRT; 365 AA. 17430 HUMAN 622911; P30452; Q9UIP7; 01-APR-1990 (Rel. 14, Created) 1. FBB-1996 (Rel. 33, Last sequence update)
                                                                                                                                                                                                                                                                                                  1A30 HUMAN

1D 1A30 HT

AC P16188,

DT 01-APR-

DT 01-FEB-
                                                                                                                                                                                                                                                                              RESULT 13
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JOINED.

AAB40048.1; AAB40048.1; AAB60651.1;

U37115; P U37114; P U19733; P

AAA83265.1; JOINED.

U37112;

EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL;

us-09-819-371-5.01i.rsp

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MEDLINE=96058597; PubMed=8522453; Krausa P., Carcassi C., Orru S., Bodmer J.G., Browning M.J., Contu L., "Defining the allelic variants of HLA-A30 in the Sardinian population using amplification refractory mutation system -- polymerase chain
                                                                                                                                               [1] —
SEQUENCE FROM N.A. (A*3001).
MEDLINE=90038496; PubMed=2476623;
Kato K., Trapani J.A., Allopenna J., Dupont B., Yang S.Y.;
Kato K., Trapani J.A., Allopenna J., Dupont B., Yang S.Y.;
Wolecular analysis of the secologically defined HLA-Aw19 antigens. A genetically distinct family of HLA-A antigens comprising A29, A31, A32, and Aw33, but probably not A30.";
J. Immunol. 143:3371-3378(1989).
                                                                                                                                                                                                                                                                                                                                           Olerup O., Daniels T.J., Barter-Lowe L., Correct sequence of the A*3001 allele obtained by PCR-SSP typing and automated nucleotide sequencing."; Tissue Antigens 44:265-267(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Diversity is demonstrated in class I HLA-A and HLA-B alleles in cameroon, Africa: description of HLA-A*03012, *2612, *3006 and HLA-B*1403, *4016, *4703.";
Issue Antigens 56:291-302(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lienert K., Russ G., Bennett G., Gao X., McCluskey J., numb.a.*3004: a new A30 allele identified in an Australian Caucasoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE OF 28-205 FROM N.A. (A*3004).
MEDLINE=96124443; PubMed=8560452;
Blasczyk R., Wehling J., Paesaler M., Hahn U., Huhn D., Salama A.;
"A novel HLA-A30 allele (A*3004) identified by single-strand
conformation polymorphism analysis and confirmed by solid-phase
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (A*3002).
MEDIINE-99056508; PubMed-1431115;
MADTINE-99056508; PubMed-1431115;
MADTINE-99056508; PubMed-1431115;
Little A.W., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
Martell R.W., du Toit E.D., Parham P.;
Martell R.W., du Toit E.D., Parham P.;
interallelic conversion: ";
J. Immunol. 149:3411-3415(1992).
   10-OCT-2003 (Rel. 42, Last annotation update)
HLA class I histocompatibility antigen, A-30 alpha chain precursor
(MHC class I antigen A*30).
                                                                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 25-279 FROM N.A. (A*3003).
MEDLINE=93209813; PubMed=8458735;
Ghoo S.Y., Starling G.C., Ansetti C., Hansen J.A.;
"Selection of an unrelated donor for marrow transplantation facilitated by the molecular characterization of a novel HLA-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 26-206 FROM N.A. (A*3006).
MEDLINE=20548605; PubMed=11098929;
Ellis J.M., Mack S.J., Leke R.F.G., Quakyi I., Johnson A.H.,
Hurley C.K.;
                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [6]
SEQUENCE OF 26-206 FROM N.A. (A*3004).
MEDLINE=96435464; PubMed=8838350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue Antigens 46:322-326(1995).
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                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (A*3001).
MEDLINE=95176329; PubMed=7871528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hum. Immunol. 44:35-42(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hum. Immunol. 36:20-26(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [5]
SEQUENCE FROM N.A. (A*3004)
                                                                           Homo sapiens (Human)
                                                                                                                                NCBI_TaxID=9606;
                                                            HLA-A OR HLAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     population.":
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                                                                                                                                                                                                                        MEDIINE=21108617; PubMed=11169261;

COX S.T., McWhinnie A.J., Koester R.P., Heine U., Holman R.,

COX S.T., McWhinnie A.J., Koester R.P., Heine U., Holman R.,

Madrigal A.J., Little A.M.;

"Further diversity at HLA-A and -B loci identified in Afro-Caribbean potential bone marrow donors.";

Tissue Artigens 57:70-72(2001).

-!- FUNCTION: Involved in the presentation of foreign antigens to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the immune system.
                                                                      Я,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBCELLULAR LOCATION: Type I membrane protein.
-!- POLYMORPHISM: The following allelee of A-30 are known: A+3001
(A30.3), A+3002, A+3003, A+3004 (A30W7), A*3006, A+3007 and A*3008. The sequence shown is that of A+3001.
                                                                            Mitton W., Koester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIMI, 142800.

R GO; GO:0005887; C:integral to plasma membrane; NAS.

R GO; GO:0005887; C:integral to plasma membrane; NAS.

R GO; GO:000555; P:immune response; NAS.

InterPro; IPR007110; Ig-like.

R InterPro; IPR003597; Ig C1.

R InterPro; IPR003006; Ig MHC.

R Pfam; PF00047; ig; 1.

R Pfam; PF0129; MHC.I: 1.

R PRINTS; PR01639; MHC.I: 1.

R PROMITS; PR0407; IG II.

R PROMITS; PR0407; IG II.

R PROSITE; PS56895; IG II.K.

R PROSITE; PS50895; IG II.K.

R PROSITE; PS60820; IG MHC.I: 1.

R PROSITE; PS60820; IG MHC.I: 1.

R PROSITE; PS60820; IG II.K.; I.

R PROSITE; PS60835; IG II.K.; I.

R PROSITE; PS60820; IG MHC.I: 1.

R PROSITE; PS60820; IG MHC.I: 1.
SEQUENCE OF 26-206 FROM N.A. (A*3007).
MEDLINE=20309230; PubMed=10852390;
Bllis J., Steiner N.K., Kosman C., Henson V.,
Ng J., Hartzman R.J., Hurley C.K.;
"Seventeen more novel HLA-A locus alleles.";
Tissue Antigens 55:369-373(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AR028714; CAASS.V4.1; -.
AR028713; AAC14191.1; -.
AF028713; AAC14191.1; -.
AF028643; AAC14191.1; JOINED.
AAC6642; AAC18600.1; -.
AAC49308; CAB57306.1; -.
AAC49310; CAB57306.1; -.
AAC49311; CAB57306.1; JOINED.
AAC49312; CAB57306.1; JOINED.
AAC49313; CAB57306.1; JOINED.
AAC49314; CAB57306.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M30556 AAAS9612 1; EMBL; C07234, AAA70162.1; EMBL; X61702, CAA43871.1; EMBL; M33657, AAA58650.1; EMBL; C34921; CAA84401.1; EMBL; U19734, AAB53658.1; EMBL; U19734, AAB53658.1; EMBL; X83770; CAA58723.1; EMBL; X83771; CAA58723.1; EMBL; X83771; CAA58723.1; ...
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PIR; 156039; 156039.
HSSP; Q95352; 1HHK.
Genew; HGNC:4931; HLA-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    microglobulin)
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EMBL;
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                                                                                                           Rizzuto G.A., Hurley C.K.;
"Novel HIA-A Allele";
"Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
-i-FUNCTION: Involved in the presentation of foreign antigens to the
                                                                                                                                                                                                                      microglobulin).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- POLYMORPHISM: The following alleles of A-36 are known: A*3601 and A*3602. The sequence shown is that of A*3601.
                                                                                                                                                                                                    -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC TAIL.
N-LINKED (GLCNAC. . .) (BY SIMILARITY)
BY SIMILARITY.
BY SIMILARITY.
Martell R.W., du Toit E.D., Parham P.;
"Distinctive HLA-A,B antigens of black populations formed by interallelic conversion."; interallelic conversion."; Immunol. 149:3411-3415(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                224 OTODIELVETRPAGDGIFOKWAAVVVPSGEEORYTCHVOHEGLP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 ÇIQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A GO (GO: 0000587) C: integral to plasma membrane; NAS. GO; GO: 0000587) C: integral to plasma membrane; NAS. GO; GO: 0000587; P: immune response; NAS. GO; GO: 0006955; P: immune response; NAS. GO; GO: 0006955; P: immune response; NAS. InterPro; IPR00110; Ig-like.

**InterPro; IPR001397; Ig-like.

**InterPro; IPR001039; MHC_I.

**Pfam; PF00047; Ig, 1.

**Pfam; PF00047; Ig, 1.

**Pfam; PF00047; Ig, 1.

**ProDom; PF00040; IG_I.

**PROSITE; PS00399; IG_INFC; 1.

**PROSITE; PS00399; IG_INFC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein; Signal; Polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V -> A (in allele A*3602).
/FTId=VAR_016610.
E -> D (in allele A*3602).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTIG=VAR 016611.
40934 MW; BA00A0085989CD3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.1%; Score 44; DB 1; Le
100.0%; Pred. No. 3.9e-38;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A-36 ALPHA
                                                                                           SEQUENCE OF 26-206 FROM N.A. (A*3602)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AF274505; AAF78082.1; --
EMBL, AP74504; AAF78082.1; JOINED.
PIR, 133478; 133478.
HSSP, Q95352; 1HHK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X61700; CAA43869.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genew; HGNC:4931; HLA-A.
MIM; 142800; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         365 AA;
                                                                                                                                                                                        immune system.
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                                                                                                                                          CYTOPLASMIC TAIL.

N-LINKED (GLCNAC. .) (BY SIMILARITY).

BY SIMILARITY.

H -> Q (in allele A*3002, allele A*3004

and allele A*3008).

FTIGHOUSE.

FTIGHOUSE.

FTIGHOUSE.

T -> A (in allele A*3008).

FTIGHOUSE.

FTIGHOUSE.

T -> A (in allele A*3006).

FTIGHOUSE.

R -> G (in allele A*3006).

FTIGHOUSE.

C -> E (in allele A*3007).

FTIGHOUSE.

C -> H (in allele A*3007).

FTIGHOUSE.

C -> H (in allele A*3007).

FTIGHOUSE.

C -> H (in allele A*3007).

FTIGHOUSE.

C -> H (in allele A*3007).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTIG=VAR_004368.

VD -> EN (in allele A*3002, allele
A*3003, allele A*3004, allele A*3006 and
allele A*3007).
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                   CLASS I HISTOCOMPATIBILITY ANTIGEN
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P30455; OPMY89;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
110-CCT-2003 (Instruction update)
110-C
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RW -> HV (in allele A*3004 and allele
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Madrigal J.A., Belich M.P., Hildebrand W.H., Benjamin R.J.,
Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TAXID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /FTId=VAR_004371.
L -> W (in allele A*3004 and allele
A*3006).
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521166D95FB1DC28 CRC64;
                                   A-30 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                             CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTIG=VAR 004370.
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ilarity 100.0%; Pred. No. 3.9
Conservative 0; Mismatches
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1A36_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (CW*0202).

MEDLINE=89235215; PubMed=2715640;

Parham P., Lawlor D.A., Lomen C.E., Ennis P.D.;

"Diversity and diversification of HLA-A,B,C alleles.";

J. Immunol. 142:3937-3950(1989).

-!- FUNCTION: Involved in the presentation of foreign antigens to the
                                                                                                                                                                                                                                                                                                                                                                                                  [1] __ SEQUENCE FROM N.A. (CW*0201).
SEQUENCE 99215297; PubMed-2708622;
MEDLINE S.A., Strachan T., Palmer M.S., McMichael A.J.;
"Complete nucleotide sequence of a unique HLA class I C locus product expressed on the human choriocarcinoma cell line BeWo.";
[2] Immunol. 142:3281-3285 (1989).
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EXTRACELIULAR ALPHA-1.

EXTRACELLULAR ALPHA-2.

CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           microglobulin).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- POLYMORPHISM: The following alleles of Cw-2 are known: Cw*0201 (Cw2.1) and Cw*0202 (Cw2.2). The sequence shown is that of Cw*0201.
                                                                           1CO2 HUMAN STANDARD; PRT; 366 AA.
P30501; P30502;
P30501; P3093 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
HLA class I histocompatibility antigen, Cw-2 alpha chain precursor (HLA-C OR HLAC.
HUMC class I antigen Cw*2).
HOME ospiens (Human)
                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID=9606;
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R EMBL; M26430; AAA59703.1; -

R HSSP; P30685; 161866.

R HSSP; P30685; 161866.

R Genew; HGNC:49313; HLA-C.

MIN; 142240.

GO; GO:0005887; C:integral to plasma membrane; NAS.

GO; GO:000585; P:immune response; NAS.

GO; GO:0005955; P:immune response; NAS.

R GO; GO:0005955; P:immune response; NAS.

R InterPro; IPR001309; Ig_c1.

R InterPro; IPR001309; MHC_I.

R InterPro; IPR001309; MHC_I.

R Pfam; PF00047; ig; 1.

R PRINTS; PR01639; MHC_I; 1.

R PRINTS; PR01639; MHC_I; 1.

R PRODON; PR000050; MHC_I; 1.

R PRODON; PR000050; MHC_I; 1.

R PRODON; PS00029; MHC_I; 1.

R PROSITE; PS50835; IG_LIKE; 1.

R PROSITE; PS50835; IG_LIKE; 1.

R MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.

R GLAMI.
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206
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                                                 N-LINKED (GLCNAC, , .) (BY SIMILARITY).
E -> A (in allele Cw*0202).
/FTId=VAR_016556.
                                                                                                                                                                                                                                                                                                                       ö
                                                                                      / r.i.c., allele Cw*0202).
/FTIG=VAR 016557.
GR -> AP [in allele Cw*0202).
/FTIG=VAR 016558.
N -> K (in allele Cw*0202).
/FTIG=VAR 016559.
E -> Q (in allele Cw*0202).
/FTIG=VAR 016560.
K -> T (in allele Cw*0202).
/FTIG=VAR 016561.
S -> C (in allele Cw*0202).
/FTIG=VAR 016561.
S -> C (in allele Cw*0202).
/FTIG=VAR 016561.
                                                                                                                                                                                                                                                                                           Score 44; DB 1; Length 366;
Pred. No. 3.9e-38;
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AD8025DEB7DA8CE6 CRC64;
             CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
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Search completed: June 18, 2004, 19:30:22 Job time: 17 secs

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June 18, 2004, 19:28:12; Search time 20 Seconds (without alignments) 1317.824 Million cell updates/sec
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274
1 GSHSLRYFSTAVSRPGRGEP......QRYTCHVQHEGLPQPLILRW 274
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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## ALIGNMENTS